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- (71) Applicant (for all designated States except US): NAU-TILUS BIOTECH [FR/FR]; 1, rue Pierre Fontaine, F-91000 EVRY (FR).
- (72) Inventors; and
- (75) Inventors/Applicants (for US only): Manuel [IT/FR]; 49, rue Félix Faure, F-91270 VI-GNEUX-SUR-SEINE (FR). DRITTANTI, Lila [IT/FR]; 49 rue Félix Faure, F-91270 VIGNEUX-SUR-SEINE (FR). FLAUX, Marjorie [FR/FR]; 38 rue Jules Vallès, F-91000 EVRY (FR).
- (74) Agents: CABINET ORES et al.; 6, avenue de Messine, F-75008 Paris (FR).

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(54) Title: MUTANT RECOMBINANT ADENO-ASSOCIATED VIRUSES RELATED APPLICATIONS

(57) Abstract: Processes and systems for the high throughput directed evolution of peptides and proteins, particularly those that act in complex biological settings, are provided. The proteins and peptides include, but are not limited to, intracellular proteins, messenger/signaling/hormone proteins and viral proteins. Also provided is a rational method for generating protein variants and also a method for titering viruses.

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# MUTANT RECOMBINANT ADENO-ASSOCIATED VIRUSES RELATED APPLICATIONS

Benefit of priority is claimed to U.S. application Serial No. 10/022,390, filed December 17, 2001, to Manuel Vega, Lila Drittanti and Marjorie Flaux entitled "MUTANT RECOMBINANT ADENO-ASSOCIATED VIRUSES." Benefit of priority is also claimed to U.S. provisional patent application serial No. 60/315,382, filed August 27, 2001, to Manuel Vega, Lila Drittanti, and Marjorie Flaux entitled "HIGH THROUGHPUT DIRECTED EVOLUTION BY RATIONAL MUTAGENESIS." Where permitted, the subject matter of each of these applications applications is incorporated in its entirety by reference thereto.

#### FIELD OF INVENTION

Mutant adeno-associated virus Rep proteins, recombinant viruses that express the proteins and nucleic acid molecule encoding the Rep proteins are provided. Uses of the recombinant viruses for treatment of diseases and vectors for gene therapy are also provided.

#### BACKGROUND

Adeno-associated virus (AAV) is a defective and non-pathogenic parvovirus that requires co-infection with either adenovirus or a herpes virus, which provide helper functions, for its growth and multiplication.

There is an extensive body of knowledge regarding AAV biology and genetics (see, *e.g.*, Weitzman *et al.* (1996) *J. Virol.* 70: 2240-2248 (1996); Walker *et al.* (1997) *J. Virol.* 71:2722-2730; Urabe *et al.* (1999)

J. Virol. 23:2682-2693; Davis et al. (2000) J. Virol. 23:74:2936-2942;Yoon et al. (2001) J. Virol. 75:3230-3239; Deng et al. (1992) Anal

25 Biochem 200:81-85; Drittanti et al. (2000) Gene Therapy 7:924-929;
Srivastava et al. (1983) J. Virol. 45:555-564; Hermonat et al. (1984) J.
Virol. 51:329-339; Chejanovsky et al. (1989) Virology 173:120-128;
Chejanovsky et al. (1990) J. Virol. 64:1764-1770; Owens et al. (1991)

Virology 184:14-22; Owens et al. (1992) J. Virol. 66:1236-1240; Qicheng Yang et al. (1992) J. Virol. 66:6058-6069; Qicheng Yang et al. (1993) J. Virol. 67:4442-4447; Owens et al. (1993) J. Virol. 62:997-1005; Sirkka et al. (1994) J. Virol. 68:2947-2957; Ramesh et al. (1995) Biochem. Biophy. Res. Com. Vol 210 (3), 717-725; Sirkka (1995) J. Virol. 69:6787-6796; Sirkka et al. (1996) Biochem. Biophy. Res. Com. 220:294-299; Ryan et al. (1996) J. Virol. 70:1542-1553; Weitzman et al. (1996) J. Virol. 70:2440-2448; Walker et al. (1997) J. Virol. 71:2722-2730; Walker et al. (1997) J. Virol. 71:6996-7004; Davis et al. (1999) J. Virol. 73:2084-2093; Urabe et al. (1999) J. Virol. 73:2682-2693; Gavin 10 et al. (1999) J. Virol. 73:9433-9445; Davis et al. (2000) J. Virol. 74:2936-2942; Pei Wu et al. (2000) J. Virol. 74:8635-8647; Alessandro Marcello et al. (2000) J. Virol. 74:9090-9098). AAV are members of the family Parvoviridae and are assigned to the genus Dependovirus. Members of this genus are small, non-enveloped, icosahedral with linear and single-stranded DNA genomes, and have been isolated from many

AAV can either remain latent after integration into host chromatin or replicate following infection. Without co-infection, AAV can enter host cells and preferentially integrate at a specific site on the q arm of chromosome 19 in the human genome.

species ranging from insects to humans.

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The AAV genome contains 4975 nucleotides and the coding sequence is flanked by two inverted terminal repeats (ITRs) on either side that are the only sequences in *cis* required for viral assembly and replication. The ITRs contain palindromic sequences, which form a hairpin secondary structure, containing the viral origins of replication. The ITRs are organized in three segments: the Rep binding site (RBS), the terminal resolution site (TRS), and a spacer region separating the RBS from the TRS.

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Regulation of AAV genes is complex and involves positive and negative regulation of viral transcription. For example, the regulatory proteins Rep 78 and Rep 68 interact with viral promoters to establish a feedback loop (Beaton et al. (1989) J. Virol 63:4450-4454; Hermonat (1994) Cancer Lett 81:129-136). Expression from the p5 and p19 promoters is negatively regulated in trans by these proteins. Rep 78 and 68, which are required for this regulation, have bind to inverted terminal repeats (ITRs; Ashktorab et al. (1989) J. Virol. 63:3034-3039) in a siteand strand-specific manner, in vivo and in vitro. This binding to ITRs induces a cleavage at the TRS and permits the replication of the hairpin structure, thus, illustrating the Rep helicase and endonuclease activities (Im et al. (1990) Cell 61:447-457; and Walker et al. (1997) J. Virol. 71:6996-7004), and the role of these non-structural proteins in the initial steps of DNA replication (Hermonat et al. (1984) J. Virol. 52:329-339). 15 Rep 52 and 40, the two minor forms of the Rep proteins, do not bind to ITRs and are dispensable for viral DNA replication and site-specific integration (Im et al. (1992) J. Virol. 66:1119-112834; Ni et al. (1994) J. Virol. 68:1128-1138.

frames (ORFs, designated left and right) that encode structural capsid proteins (Cap) and non-structural proteins (Rep). There are three promoters: p5 (from nucleotides 255 to 261: TATTTAA), p19 (from nucleotide 843 to 849: TATTTAA) and p40 (from nucleotides 1822 to 1827: ATATAA). The right-side ORF (see FIG. 1) encodes three capsid structural proteins (Vp 1-3). These three proteins, which are encoded by overlapping DNA, result from differential splicing and the use of an unusual initiator codon (Cassinoti et al. (1988) Virology 167:176-184). Expression of the capsid genes is regulated by the p40 promoter. Capsid proteins VP1, VP2 and VP3 initiate from the p40 promoter. VP1 uses an

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alternate splice acceptor at nucleotide 2201; whereas VP2 and VP3 are derived from the same transcription unit, but VP2 use an ACG triplet as an initiation codon upstream from the start of VP3. On the left side of the genome, two promoters p5 and p19 direct expression of four regulatory proteins. The left flanking sequence also uses a differential splicing mechanism (Mendelson et al. (1986) J. Virol 60:823-832) to encode the Rep proteins, designated Rep 78, 68, 52 and 40 on the basis molecular weight. Rep 78 and 68 are translated from a transcript produced from the p5 promoter and are produced from the unspliced and spliced form, respectively, of the transcript. Rep 52 and 40 are the translation products of unspliced and spliced transcripts from the p19 promoter.

AAV and rAAV have many applications, including use as a gene transfer vector, for introducing heterologous nucleic acid into cells and for genetic therapy. Advances in the production of high-titer rAAV stocks to 15 the transition to human clinical trials have been made, but improvement of rAAV production will be complemented with special attention to clinical applications of rAAV vectors as a successful gene therapy approach. Productivity of rAAV (i.e. the amount of vector particles that can be 20 obtained per unitary manufacturing operation) is one of the rate limiting steps in the further development of rAAV as gene therapy vector. Methods for high throughput production and screening of rAAV have been developed (see, e.g., Drittanti et al. (2000) Gene Therapy 7:924-929). Briefly, as with the other steps in methods provided herein, the plasmid preparation, transfection, virus productivity and titer and biological activity assessment are intended to be performed in an automatable high throughput format, such as in a 96 well or loci formats (or other number of wells or multiples of 96, such as 384, 1536 . . . 9600, 9984 . . well or loci formats).

#### SUMMARY

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Mutant AAV Rep proteins, nucleic acid molecules encoding such proteins, and rAAV that encode the proteins are provided. Among the rep proteins are those that result in increased rAAV production in rAAV that encode such mutants, thereby, among a variety of advantages, offering a solution to the need in the gene therapy industry to increase the production of therapeutic vectors without up-scaling manufacturing. Methods of gene therapy using the rAAV are provided.

Directed evolution methods provided in co-pending U.S. provisional application Serial No. 60/315,382, filed as U.S. application Serial No. 10/022,249, and described herein have been used to identify amino acid "hit" positions in adeno-associated virus (AAV) rep proteins that are relevant for AAV or rAAV production. Those amino acid positions are selected such that a change in the amino acid leads to a change in protein activity either to lower activity or to higher activity compared to native-sequence Rep proteins. The hit positions were then used to generate further mutants designated "leads." Provided herein are the resulting mutant rep proteins that result in either higher or lower levels of AAV or rAAV virus compared to the wild-type (native) Rep protein(s). Nucleic acid molecules that encode the mutant Rep proteins are also provided.

Also provided are rAAV that contain the nucleic acid molecules and methods that use the rAAV to produce the mutant Rep. Cell-free (in vitro) and intracellular methods are provided. Cells containing the rAAV are also provided.

Among the Rep mutants provided herein, in addition to Rep mutants that enhance AAV production, are those that inhibit papillomavirus (PV) and PV-associated diseases, including certain cancers and human immunodeficiency virus (HIV) and HIV-associated diseases. Methods of treating such diseases are provided.

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#### **DESCRIPTION OF THE FIGURES**

FIGURE 1 shows the genetic map of AAV, including the location of promoters, and transcripts; amino acid 1 of the Rep 78 gene is at nucleotide 321 in the AAV-2 genome.

FIGURES 2A and 2B depict "HITS" and "LEADS" respectively for identification of AAV rep mutants "evolved" for increased activity.

FIGURES 3A and 3B show the alignment of amino acid sequences of Rep78 among AAV-1; AAV-6; AAV-3; AAV-3B; AAV-4; AAV-2; AAV-5 sequences, respectively; the hit positions with 100 percent homology among the serotypes are bolded italics, where the position is different (compared to AAV-2, no. 6 in the Figure) in a particular serotype, it is in bold; a sequence indicating relative conservation of sequences among the serotypes is labeled "C".

#### Legend:

1 is AAV-1; 2 is AAV-6, 3 is AAV-3, 4 is AAV-3B, 5 is AAV-4, 6 is AAV-2, and 7 is AAV-5;
"." where the amino acid is present ≥ 20%;
":" where the amino acid is present ≥ 40%;
"+" where the amino acid is present ≥ 60%;
"\*" where the amino acid is present ≥ 80%; and where the amino acid is the same amongst all serotypes depicted it is represented by its single letter code.

#### DETAILED DESCRIPTION

#### 25 A. Definitions

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Unless defined otherwise, all technical and scientific terms used herein have the same meaning as is commonly understood by one of skill in the art to which this invention belongs. All patents, patent applications, published applications and publications, Genbank sequences, websites and other published materials referred to throughout the entire disclosure herein are, unless noted otherwise, incorporated by reference

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in their entirety. In the event that there are a plurality of definitions for terms herein, those in this section prevail.

As used herein, directed evolution refers to methods that adapt natural proteins or protein domains to work in new chemical or biological environments and/or to elicit new functions. It is more a more broadbased technology than DNA shuffling.

As used herein, high-throughput screening (HTS) refers to processes that test a large number of samples, such as samples of test proteins or cells containing nucleic acids encoding the proteins of interest to identify structures of interest or to identify test compounds that interact with the variant proteins or cells containing them. HTS operations are amenable to automation and are typically computerized to handle sample preparation, assay procedures and the subsequent processing of large volumes of data.

As used herein, DNA shuffling is a PCR-based technology that produces random rearrangements between two or more sequence-related genes to generate related, although different, variants of given gene.

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As used herein, "hits" are mutant proteins that have an alteration in any attribute, chemical, physical or biological property in which such alteration is sought. In the methods herein, hits are generally generated by systematically replacing each amino acid in a protein or a domain thereof with a selected amino acid, typically Alanine, Glycine, Serine or any amino acid, as long as each residue is replaced with the same residue. Hits may be generated by other methods known to those of skill in the art tested by the high-throughput methods herein. For purposes herein a Hit typically has activity with respect to the function of interest that differs by at least 10%, 20%, 30% or more from the wild type or native protein. The desired alteration, which is generally a reduction in activity, will depend upon the function or property of interest.

As used herein, "leads" are "hits" whose activity has been optimized for the particular attribute, chemical, physical or biological property. In the methods herein, leads are generally produced by systematically replacing the hit loci with all remaining 18 amino acids, and 5 identifying those among the resulting proteins that have a desired activity. The leads may be further optimized by replacement of a plurality of "hit" residues. Leads may be generated by other methods known to those of skill in the art and tested by the highthroughput methods herein. For purposes herein a lead typically has activity with respect to the function 10 of interest that differs from the native activity, by a desired amount and is at by at least 10%, 20%, 30% or more from the wild type or native protein. Generally a Lead will have an activity that is 2 to 10 or more times the native protein for the activity of interest. As with hits, the change in the activity is dependent upon the activity that is "evolved." 15 The desired alteration will depend upon the function or property of interest.

As used herein, MOI is multiplicity of infection.

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As used herein, ip, with reference to a virus or recombinant vector, refers to a titer of infectious particles.

As used herein, pp refers to the total number of vector (or virus) physical particles

As used herein, biological and pharmacological activity includes any activity of a biological pharmaceutical agent and includes, but is not limited to, biological efficiency, transduction efficiency, gene/transgene expression, differential gene expression and induction activity, titer, progeny productivity, toxicity, citotoxicity, immunogenicity, cell proliferation and/or differentiation activity, anti-viral activity, morphogenetic activity, teratogenetic activity, pathogenetic activity, therapeutic activity, tumor supressor activity, ontogenetic activity,

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oncogenetic activity, enzymatic activity, pharmacological activity, cell/tissue tropism and delivery.

As used herein, "output signal" refers to parameters that can be followed over time and, if desired, quantified. For example, when a virus 5 infects or is introduced into a cell, the cell containing the virus undergoes a number of changes. Any such change that can be monitored and used to assess infection, is an output signal, and the cell is referred to as a reporter cell; the encoding nucleic acid is referred to as a reporter gene, and the construct that includes the encoding nucleic acid is a reporter 10 construct. Output signals include, but are not limited to, enzyme activity, fluorescence, luminescence, amount of product produced and other such signals. Output signals include expression of a viral gene or viral gene product, including heterologous genes (transgenes) inserted into the virus. Such expression is a function of time ("t") after infection, which in turn is related to the amount of virus used to infect the cell, and, hence, the concentration of virus ("s") in the infecting composition. For higher concentrations the output signal is higher. For any particular concentration, the output signal increases as a function of time until a plateau is reached. Output signals may also measure the interaction between cells, expressing heterologous genes, and biological agents

As used herein, adeno-associated virus (AAV) is a defective and non-pathogenic parvovirus that requires co-infection with either adenovirus or herpes virus for its growth and multiplication, able of providing helper functions. A variety of serotypes are known, and contemplated herein. Such serotypes include, but are not limited to: AAV-1 (Genbank accession no. NC002077; accession no. VR-645); AAV-2 (Genbank accession no. NC001401; accession no. VR-680); AAV-3 (Genbank accession no. NC001729; accession no. VR-681); AAV-3b (Genbank accession no. NC001863); AAV-4 (Genbank accession no.

NC001829; ATCC accession no. VR-646); AAV-6 (Genbank accession no.NC001862); and avian associated adeno-virus (ATCC accession no. VR-1449). The preparation and use of AAVs as vectors for gene expression *in vitro* and for *in vivo* use for gene therapy are well known (see, e.g., U.S. Patent Nos. 4,797,368, 5,139,941, 5,798,390 and 6,127,175; Tessier et al. (2001) J. Virol. 75:375-383; Salvetti et al. (1998) Hum Gene Ther 20:695-706; Chadeuf et al. (2000) J Gene Med 2:260-268).

As used herein, the activity of a Rep protein or of a capsid protein refers to any biological activity that can be assessed. In particular, herein, the activity assessed for the rep proteins is the amount (i.e., titer) of AAV produced by a cell.

As used herein, the Hill equation is a mathematical model that relates the concentration of a drug (i.e., test compound or substance) to the response being measured

$$y = \frac{V_{max}[D]^x}{[D]^n + [D_{50}]^n}$$

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where y is the variable being measured, such as a response, signal,  $y_{max}$  is the maximal response achievable, [D] is the molar concentration of a drug, [D<sub>50</sub>] is the concentration that produces a 50% maximal response to the drug, n is the slope parameter, which is 1 if the drug binds to a single site and with no cooperativity between or among sites. A Hill plot is  $log_{10}$  of the ratio of ligand-occupied receptor to free receptor vs. log [D] (M). The slope is n, where a slope of greater than 1 indicates cooperativity among binding sites, and a slope of less than 1 can indicate heterogeneity of binding. This general equation has been employed for assessing interactions in complex biological systems (see, published International

PCT application No. WO 01/44809 based on PCT n° PCT/FR00/03503, see, also, EXAMPLES).

As used herein, in the Hill-based analysis (published International PCT application No. WO 01/44809 based on PCT n° PCT/FR00/03503), the parameters,  $\pi, \kappa, \tau, \epsilon, \eta, \theta$ , are as follows:

- $\pi$  potency of the biological agent acting on the assay (cell-based) system;
- K constant of resistance of the assay system to elicit a response to a biological agent;
- 10  $\epsilon$  is global efficiency of the process or reaction triggered by the biological agent on the assay system;

r is the apparent titer of the biological agent;

heta is the absolute titer of the biological agent; and

 $\eta$  is the heterogeneity of the biological process or reaction.

In particular, as used herein, the parameters  $\pi$  (potency) or  $\kappa$  (constant of resistance) are used to respectively assess the potency of a test agent to produce a response in an assay system and the resistance of the assay system to respond to the agent.

As used herein,  $\epsilon$ (efficiency), is the slope at the inflection point of the Hill curve (or, in general, of any other sigmoidal or linear approximation), to assess the efficiency of the global reaction (the biological agent and the assay system taken together) to elicit the biological or pharmacological response.

As used herein, r (apparent titer) is used to measure the limiting dilution or the apparent titer of the biological agent.

As used herein,  $\theta$  (absolute titer), is used to measure the absolute limiting dilution or titer of the biological agent.

As used herein,  $\eta$  (heterogeneity) measures the existence of discontinuous phases along the global reaction, which is reflected by an

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abrupt change in the value of the Hill coefficient or in the constant of resistance.

As used herein, a library of mutants refers to a collection of plasmids or other vehicles that carry (encode) the gene variants, such that individual plasmids or other vehicles carry individual gene variants.

When a library of proteins is contemplated, it will be so-stated.

As used herein, a "reporter cell" is the cell that "reports", *i.e.*, undergoes the change, in response to introduction of the nucleic acid infection and, therefore, it is named here a reporter cell.

As used herein, "reporter" or "reporter moiety" refers to any moiety that allows for the detection of a molecule of interest, such as a protein expressed by a cell. Reporter moieties include, but are not limited to, for example, fluorescent proteins, such as red, blue and green fluorescent proteins; lacZ and other detectable proteins and gene products. For expression in cells, nucleic acid encoding the reporter moiety can be expressed as a fusion protein with a protein of interest or under the control of a promoter of interest.

As used herein, a titering virus increases or decreases the output signal from a reporter virus, which is a virus that can be detected, such as by a detectable label or signal.

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As used herein, phenotype refers to the physical, physiological or other manifestation of a genotype (a sequence of a gene). In methods herein, phenotypes that result from alteration of a genotype are assessed.

As used herein, activity refers to the function or property to be evolved. An active site refers to a site(s) responsible or that participates in conferring the activity or function. The activity or active site evolved (the function or property and the site conferring or participating in conferring the activity) may have nothing to do with natural activities of

a protein. For example, it could be an 'active site' for conferring immunogenicity (immunogenic sites or epitopes) on a protein.

As used herein, the amino acids, which occur in the various amino acid sequences appearing herein, are identified according to their known, three-letter or one-letter abbreviations (see, Table 1). The nucleotides, which occur in the various nucleic acid fragments, are designated with the standard single-letter designations used routinely in the art.

As used herein, amino acid residue refers to an amino acid formed upon chemical digestion (hydrolysis) of a polypeptide at its peptide

10 linkages. The amino acid residues described herein are presumed to be in the "L" isomeric form. Residues in the "D" isomeric form, which are sodesignated, can be substituted for any L-amino acid residue, as long as the desired functional property is retained by the polypeptide. NH<sub>2</sub> refers to the free amino group present at the amino terminus of a polypeptide.

15 COOH refers to the free carboxy group present at the carboxyl terminus of a polypeptide. In keeping with standard polypeptide nomenclature described in *J. Biol. Chem., 243*:3552-59 (1969) and adopted at 37 C.F.R. § § 1.821 - 1.822, abbreviations for amino acid residues are shown in the following Table:

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Table 1
Table of Correspondence

SYMBOL		
1-Letter	3-Letter	AMINO ACID
Y	Tyr	tyrosine
G	Gly	glycine
F	Phe	phenylalanine
М	Met	methionine
Α	Ala	alanine
S	Ser	serine

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SYMBOL		
1 .	lle	isoleucine
L	Leu	leucine
T	Thr	threonine
٧	Val	valine
Р	Pro	proline
К	Lγs	lysine
Н	His	histidine
Q	Gln	glutamine
E	Glu	glutamic acid
Z	Glx	Glu and/or Gln
W	Trp	tryptophan
R	Arg	arginine
D	Asp	aspartic acid
Ν	Asn	asparagine
В	Asx	Asn and/or Asp
С	Cys	cysteine
Х	Xaa	Unknown or other

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represented herein by formulae have a left to right orientation in the conventional direction of amino-terminus to carboxyl-terminus. In addition, the phrase "amino acid residue" is broadly defined to include the amino acids listed in the Table of Correspondence and modified and unusual amino acids, such as those referred to in 37 C.F.R. § § 1.821-1.822, and incorporated herein by reference. Furthermore, it should be noted that a dash at the beginning or end of an amino acid residue sequence indicates a peptide bond to a further sequence of one or more

amino acid residues or to an amino-terminal group such as  $NH_2$  or to a carboxyl-terminal group such as COOH.

In a peptide or protein, suitable conservative substitutions of amino acids are known to those of skill in this art and may be made generally without altering the biological activity of the resulting molecule. Those of skill in this art recognize that, in general, single amino acid substitutions in non-essential regions of a polypeptide do not substantially alter biological activity (see, e.g., Watson et al. *Molecular Biology of the Gene*, 4th Edition, 1987, The Benjamin/Cummings Pub. co., p.224).

Such substitutions are preferably made in accordance with those set forth in TABLE 2 as follows:

TABLE 2

	17.522 2	
	Original residue Ala (A)	Conservative substitution Gly; Ser
15	Arg (R)	Lys
	Asn (N)	Gln; His
	Cys (C)	Ser
	Gin (Q)	Asn
	Glu (E)	Asp
20	Gly (G)	Ala; Pro
	His (H)	Asn; Gln
	lle (I)	Leu; Val
	Leu (L)	lle; Val
	Lys (K)	Arg; Gln; Glu
25	Met (M)	Leu; Tyr; lle
	Phe (F)	Met; Leu; Tyr
	Ser (S)	Thr
	Thr (T)	Ser
	Trp (W)	Туг
30	Tyr (Y)	Trp; Phe
	Val (V)	lle: Leu

Other substitutions are also permissible and may be determined empirically or in accord with known conservative substitutions.

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As used herein, nucleic acids include DNA, RNA and analogs thereof, including protein nucleic acids (PNA) and mixture thereof.

Nucleic acids can be single or double stranded. When referring to probes

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or primers, optionally labeled, with a detectable label, such as a fluorescent or radiolabel, single-stranded molecules are contemplated. Such molecules are typically of a length such that they are statistically unique of low copy number (typically less than 5, preferably less than 3) for probing or priming a library. Generally a probe or primer contains at least 14, 16 or 30 contiguous of sequence complementary to or identical to a gene of interest. Probes and primers can be 10, 14, 16, 20, 30, 50, 100 or more nucleic acid bases long.

As used herein, homologous means about greater than 25% nucleic acid sequence identity, preferably 25% 40%, 60%, 80%, 90% or 95%. The intended percentage will be specified. The terms "homology" and "identity" are often used interchangeably. In general, sequences are aligned so that the highest order match is obtained (see, e.g.: Computational Molecular Biology, Lesk, A.M., ed., Oxford University Press, New York, 1988; Biocomputing: Informatics and Genome Projects, Smith, D.W., ed., Academic Press, New York, 1993; Computer Analysis of Sequence Data, Part I, Griffin, A.M., and Griffin, H.G., eds., Humana Press, New Jersey, 1994; Sequence Analysis in Molecular Biology, von Heinje, G., Academic Press, 1987; and Sequence Analysis Primer, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, 1991; Carillo et al. (1988) SIAM J Applied Math 48:1073). By sequence identity, the number of conserved amino acids are determined by standard alignment algorithms programs, and are used with default gap penalties established by each supplier. Substantially homologous nucleic acid 25 molecules would hybridize typically at moderate stringency or at high stringency all along the length of the nucleic acid of interest. Also contemplated are nucleic acid molecules that contain degenerate codons in place of codons in the hybridizing nucleic acid molecule.

As used herein, a nucleic acid homolog refers to a nucleic acid that includes a preselected conserved nucleotide sequence, such as a sequence encoding a therapeutic polypeptide. By the term "substantially homologous" it is meant having at least 80%, preferably at least 90%, most preferably at least 95% homology therewith or a less percentage of homology or identity and conserved biological activity or function.

The terms "homology" and "identity" are often used interchangeably. In this regard, percent homology or identity may be determined, for example, by comparing sequence information using a GAP 10 computer program. The GAP program uses the alignment method of Needleman and Wunsch (J. Mol. Biol. 48:443 (1970), as revised by Smith and Waterman (Adv. Appl. Math. 2:482 (1981). Briefly, the GAP program defines similarity as the number of aligned symbols (i.e., nucleotides or amino acids) which are similar, divided by the total number of symbols in 15 the shorter of the two sequences. The preferred default parameters for the GAP program may include: (1) a unary comparison matrix (containing a value of 1 for identities and 0 for non-identities) and the weighted comparison matrix of Gribskov and Burgess, Nucl: Acids Res. 14:6745 (1986), as described by Schwartz and Dayhoff, eds., ATLAS OF PROTEIN 20 SEQUENCE AND STRUCTURE, National Biomedical Research Foundation, pp. 353-358 (1979); (2) a penalty of 3.0 for each gap and an additional 0.10 penalty for each symbol in each gap; and (3) no penalty for end gaps.

Whether any two nucleic acid molecules have nucleotide sequences that are, for example, at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99%, "identical" can be determined using known computer algorithms such as the "FAST A" program, using for example, the default parameters as in Pearson and Lipman, *Proc. Natl. Acad. Sci. USA 85*:2444 (1988).

Alternatively the BLAST function of the National Center for Biotechnology Information database may be used to determine identity

In general, sequences are aligned so that the highest order match is obtained. "Identity" per se has an art-recognized meaning and can be 5 calculated using published techniques. (See, e.g.: Computational Molecular Biology, Lesk, A.M., ed., Oxford University Press, New York, 1988; Biocomputing: Informatics and Genome Projects, Smith, D.W., ed., Academic Press, New York, 1993; Computer Analysis of Sequence Data, Part I, Griffin, A.M., and Griffin, H.G., eds., Humana Press, New Jersey, 10 1994; Sequence Analysis in Molecular Biology, von Heinje, G., Academic Press, 1987; and Sequence Analysis Primer, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, 1991). While there exist a number of methods to measure identity between two polynucleotide or polypeptide sequences, the term "identity" is well known to skilled artisans (Carillo, H. & Lipton, D., SIAM J Applied Math 48:1073 (1988)). Methods commonly employed to determine identity or similarity between two sequences include, but are not limited to, those disclosed in Guide to Huge Computers, Martin J. Bishop, ed., Academic Press, San Diego, 1994, and Carillo, H. & Lipton, D., SIAM J Applied Math 48:1073 20 (1988). Methods to determine identity and similarity are codified in computer programs. Preferred computer program methods to determine identity and similarity between two sequences include, but are not limited to, GCG program package (Devereux, J., et al., Nucleic Acids Research 12//):387 (1984)), BLASTP, BLASTN, FASTA (Atschul, S.F., et al., J Molec Biol 215:403 (1990)), and CLUSTALW. For sequences displaying a relatively high degree of homology, alignment can be effected manually by simpling lining up the sequences by eye and matching the conserved portions.

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Therefore, as used herein, the term "identity" represents a comparison between a test and a reference polypeptide or polynucleotide. For example, a test polypeptide may be defined as any polypeptide that is 90% or more identical to a reference polypeptide.

For the alignments presented herein (see, Figures 3A and 3B) for the AAV serotype, the CLUSTALW program was employed with parameters set as follows: scoring matrix BLOSUM, gap open 10, gap extend 0.1, gap distance 40% and transitions/transversions 0.5; specific residue penalties for hydrophobic amino acids (DEGKNPQRS), distance 10 between gaps for which the penalties are augmented was 8, and gaps of externeties penalized less than internal gaps.

As used herein, a "corresponding" position on a protein, such as the AAV rep protein, refers to an amino acid position based upon alignment to maximize sequence identity. For AAV Rep proteins an \* alignment of the Rep 78 protein from AAV-2 and the corresponding protein from other AAV serotypes (AAV-1, AAV-6, AAV-3, AAV-3B, AAV-4, AAV-2 and AAV-5) is shown in Figures 3A and 3B. The "hit" positions are shown in italics.

As used herein, the term at least "90% identical to" refers to 20 percent identities from 90 to 100% relative to the reference polypeptides. Identity at a level of 90% or more is indicative of the fact that, assuming for exemplification purposes a test and reference polynucleotide length of 100 amino acids are compared. No more than 10% (i.e., 10 out of 100) amino acids in the test polypeptide differs from that of the reference 25 polypeptides. Similar comparisons may be made between a test and reference polynucleotides. Such differences may be represented as point mutations randomly distributed over the entire length of an amino acid sequence or they may be clustered in one or more locations of varying length up to the maximum allowable, e.g. 10/100 amino acid difference

(approximately 90% identity). Differences are defined as nucleic acid or amino acid substitutions, or deletions.

As used herein, it is also understood that the terms substantially identical or similar varies with the context as understood by those skilled in the relevant art.

As used herein, genetic therapy involves the transfer of heterologous nucleic acids to the certain cells, target cells, of a mammal, particularly a human, with a disorder or conditions for which such therapy is sought. The nucleic acid, such as DNA, is introduced into the selected target cells in a manner such that the heterologous nucleic acid, such as DNA, is expressed and a therapeutic product encoded thereby is produced. Alternatively, the heterologous nucleic acid, such as DNA, may in some manner mediate expression of DNA that encodes the therapeutic product, or it may encode a product, such as a peptide or RNA that in some manner mediates, directly or indirectly, expression of a 15 therapeutic product. Genetic therapy may also be used to deliver nucleic acid encoding a gene product that replaces a defective gene or supplements a gene product produced by the mammal or the cell in which it is introduced. The introduced nucleic acid may encode a therapeutic 20 compound, such as a growth factor or inhibitor thereof, or a tumor necrosis factor or inhibitor thereof, such as a receptor therefor, that is not normally produced in the mammalian host or that is not produced in therapeutically effective amounts or at a therapeutically useful time. The heterologous nucleic acid, such as DNA, encoding the therapeutic product 25 may be modified prior to introduction into the cells of the afflicted host in order to enhance or otherwise alter the product or expression thereof. Genetic therapy may also involve delivery of an inhibitor or repressor or other modulator of gene expression.

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As used herein, heterologous or foreign nucleic acid, such as DNA and RNA, are used interchangeably and refer to DNA or RNA that does not occur naturally as part of the genome in which it is present or which is found in a location or locations in the genome that differ from that in 5 which it occurs in nature. Heterologous nucleic acid is generally not endogenous to the cell into which it is introduced, but has been obtained from another cell or prepared synthetically. Generally, although not necessarily, such nucleic acid encodes RNA and proteins that are not normally produced by the cell in which it is expressed. Any DNA or RNA 10 that one of skill in the art would recognize or consider as heterologous or foreign to the cell in which it is expressed is herein encompassed by heterologous DNA. Heterologous DNA and RNA may also encode RNA or proteins that mediate or alter expression of endogenous DNA by affecting transcription, translation, or other regulatable biochemical processes. 15 Examples of heterologous nucleic acid include, but are not limited to, nucleic acid that encodes traceable marker proteins, such as a protein that confers drug resistance, nucleic acid that encodes therapeutically

Hence, herein heterologous DNA or foreign DNA, includes a DNA molecule not present in the exact orientation and position as the counterpart DNA molecule found in the genome. It may also refer to a DNA molecule from another organism or species (*i.e.*, exogenous).

and DNA that encodes other types of proteins, such as antibodies.

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effective substances, such as anti-cancer agents, enzymes and hormones,

As used herein, a therapeutically effective product introduced by genetic therapy is a product that is encoded by heterologous nucleic acid, typically DNA, that, upon introduction of the nucleic acid into a host, a product is expressed that ameliorates or eliminates the symptoms, manifestations of an inherited or acquired disease or that cures the disease.

As used herein, a therapeutically effective dose refers to that amount of the compound sufficient to result in amelioration of symptoms of disease.

As used herein, isolated with reference to a nucleic acid molecule or polypeptide or other biomolecule means that the nucleic acid or polypeptide has separated from the genetic environment from which the polypeptide or nucleic acid were obtained. It may also mean altered from the natural state. For example, a polynucleotide or a polypeptide naturally present in a living animal is not "isolated," but the same polynucleotide or polypeptide separated from the coexisting materials of its natural state is "isolated", as the term is employed herein. Thus, a polypeptide or polynucleotide produced and/or contained within a recombinant host cell is considered isolated. Also intended as an "isolated polypeptide" or an "isolated polynucleotide" are polypeptides or polynucleotides that have been purified, partially or substantially, from a recombinant host cell or from a native source. For example, a recombinantly produced version of a compounds can be substantially purified by the one-step method described in Smith and Johnson, Gene 67:31-40 (1988). The terms isolated and purified are sometimes used interchangeably.

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Thus, by "isolated" it is meant that the nucleic is free of the coding sequences of those genes that, in the naturally-occurring genome of the organism (if any), immediately flank the gene encoding the nucleic acid of interest. Isolated DNA may be single-stranded or double-stranded, and may be genomic DNA, cDNA, recombinant hybrid DNA, or synthetic DNA. It may be identical to a native DNA sequence, or may differ from such sequence by the deletion, addition, or substitution of one or more nucleotides.

Isolated or purified as it refers to preparations made from biological cells or hosts means any cell extract containing the indicated DNA or

protein including a crude extract of the DNA or protein of interest. For example, in the case of a protein, a purified preparation can be obtained following an individual technique or a series of preparative or biochemical techniques and the DNA or protein of interest can be present at various degrees of purity in these preparations. The procedures may include for example, but are not limited to, ammonium sulfate fractionation, gel filtration, ion exchange change chromatography, affinity chromatography, density gradient centrifugation and electrophoresis.

A preparation of DNA or protein that is "substantially pure" or "isolated" should be understood to mean a preparation free from naturally occurring materials with which such DNA or protein is normally associated in nature. "Essentially pure" should be understood to mean a "highly" purified preparation that contains at least 95% of the DNA or protein of interest.

A cell extract that contains the DNA or protein of interest should be understood to mean a homogenate preparation or cell-free preparation obtained from cells that express the protein or contain the DNA of interest. The term "cell extract" is intended to include culture media, especially spent culture media from which the cells have been removed.

As used herein, receptor refers to a biologically active molecule that specifically binds to (or with) other molecules. The term "receptor protein" may be used to more specifically indicate the proteinaceous nature of a specific receptor.

As used herein, recombinant refers to any progeny formed as the result of genetic engineering.

As used herein, a promoter region refers to the portion of DNA of a gene that controls transcription of the DNA to which it is operatively linked. The promoter region includes specific sequences of DNA that are sufficient for RNA polymerase recognition, binding and transcription

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initiation. This portion of the promoter region is referred to as the promoter. In addition, the promoter region includes sequences that modulate this recognition, binding and transcription initiation activity of the RNA polymerase. These sequences may be cis acting or may be 5 responsive to trans acting factors. Promoters, depending upon the nature of the regulation, may be constitutive or regulated.

As used herein, the phrase "operatively linked" generally means the sequences or segments have been covalently joined into one piece of DNA, whether in single or double stranded form, whereby control or 10 regulatory sequences on one segment control or permit expression or replication or other such control of other segments. The two segments are not necessarily contiguous. For gene expression a DNA sequence and a regulatory sequence(s) are connected in such a way to control or permit gene expression when the appropriate molecules, e.g., transcriptional activator proteins, are bound to the regulatory sequence(s).

As used herein, production by recombinant means by using recombinant DNA methods means the use of the well known methods of molecular biology for expressing proteins encoded by cloned DNA, including cloning expression of genes and methods, such as gene shuffling and phage display with screening for desired specificities.

As used herein, a splice variant refers to a variant produced by differential processing of a primary transcript of genomic DNA that results in more than one type of mRNA.

As used herein, a composition refers to any mixture of two or more 25 products or compounds. It may be a solution, a suspension, liquid, powder, a paste, aqueous, non-aqueous or any combination thereof.

As used herein, a combination refers to any association between two or more items.

As used herein, substantially identical to a product means sufficiently similar so that the property of interest is sufficiently unchanged so that the substantially identical product can be used in place of the product.

As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of preferred vector is an episome, i.e., a nucleic acid capable of 10 extra-chromosomal replication. Preferred vectors are those capable of autonomous replication and/or expression of nucleic acids to which they are linked. Vectors capable of directing the expression of genes to which they are operatively linked are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques 15 are often in the form of "plasmids" which refer generally to circular double stranded DNA loops which, in their vector form, are not bound to the chromosome. "Plasmid" and "vector" are used interchangeably as the plasmid is the most commonly used form of vector. Other such other forms of expression vectors that serve equivalent functions and that become known in the art can be used subsequently hereto.

As used herein, vector is also used interchangeable with "virus vector" or "viral vector". In this case, which will be clear from the context, the "vector" is not self-replicating. Viral vectors are engineered viruses that are operatively linked to exogenous genes to transfer (as vehicles or shuttles) the exogenous genes into cells.

As used herein, transduction refers to the process of gene transfer and expression into mammalian and other cells mediated by viruses. Transfection refers to the process when mediated by plasmids.

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As used herein, "polymorphism" refers to the coexistence of more than one form of a gene or portion thereof. A portion of a gene of which there are at least two different forms, i.e., two different nucleotide sequences, is referred to as a "polymorphic region of a gene". A polymorphic region can be a single nucleotide, referred to as a single nucleotide polymorphism (SNP), the identity of which differs in different alleles. A polymorphic region can also be several nucleotides in length.

As used herein, "polymorphic gene" refers to a gene having at least one polymorphic region.

As used herein, "allele", which is used interchangeably herein with "allelic variant" refers to alternative forms of a gene or portions thereof. Alleles occupy the same locus or position on homologous chromosomes. When a subject has two identical alleles of a gene, the subject is said to be homozygous for the gene or allele. When a subject has two different alleles of a gene, the subject is said to be heterozygous for the gene. Alleles of a specific gene can differ from each other in a single nucleotide, or several nucleotides, and can include substitutions, deletions, and insertions of nucleotides. An allele of a gene can also be a form of a gene containing a mutation.

As used herein, the term "gene" or "recombinant gene" refers to a nucleic acid molecule comprising an open reading frame and including at least one exon and (optionally) an intron sequence. A gene can be either RNA or DNA. Genes may include regions preceding and following the coding region (leader and trailer).

As used herein, "intron" refers to a DNA sequence present in a given gene which is spliced out during mRNA maturation.

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As used herein, "nucleotide sequence complementary to the nucleotide sequence set forth in SEQ ID NO: x" refers to the nucleotide sequence of the complementary strand of a nucleic acid strand having

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SEQ ID NO: x. The term "complementary strand" is used herein interchangeably with the term "complement". The complement of a nucleic acid strand can be the complement of a coding strand or the complement of a non-coding strand. When referring to double stranded nucleic acids, the complement of a nucleic acid having SEQ ID NO: x refers to the complementary strand of the strand having SEQ ID NO: x or to any nucleic acid having the nucleotide sequence of the complementary strand of SEQ ID NO: x. When referring to a single stranded nucleic acid having the nucleotide sequence SEQ ID NO: x, the complement of this nucleic acid is a nucleic acid having a nucleotide sequence which is complementary to that of SEQ ID NO: x.

As used herein, the term "coding sequence" refers to that portion of a gene that encodes an amino acid sequence of a protein.

As used herein, the term "sense strand" refers to that strand of a double-stranded nucleic acid molecule that has the sequence of the mRNA that encodes the amino acid sequence encoded by the double-stranded nucleic acid molecule.

As used herein, the term "antisense strand" refers to that strand of a double-stranded nucleic acid molecule that is the complement of the sequence of the mRNA that encodes the amino acid sequence encoded by the double-stranded nucleic acid molecule.

As used herein, an array refers to a collection of elements, such as nucleic acid molecules, containing three or more members. An addressable array is one in which the members of the array are identifiable, typically by position on a solid phase support or by virtue of an identifiable or detectable label, such as by color, fluorescence, electronic signal (i.e. RF, microwave or other frequency that does not substantially alter the interaction of the molecules of interest), bar code or other symbology, chemical or other such label. Hence, in general the

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members of the array are immobilized to discrete identifiable loci on the surface of a solid phase or directly or indirectly linked to or otherwise associated with the identifiable label, such as affixed to a microsphere or other particulate support (herein referred to as beads) and suspended in solution or spread out on a surface.

As used herein, a support (also referred to as a matrix support, a matrix, an insoluble support or solid support) refers to any solid or semisolid or insoluble support to which a molecule of interest, typically a biological molecule, organic molecule or biospecific ligand is linked or 10 contacted. Such materials include any materials that are used as affinity matrices or supports for chemical and biological molecule syntheses and analyses, such as, but are not limited to: polystyrene, polycarbonate, polypropylene, nylon, glass, dextran, chitin, sand, pumice, agarose, polysaccharides, dendrimers, buckyballs, polyacrylamide, silicon, rubber, and other materials used as supports for solid phase syntheses, affinity separations and purifications, hybridization reactions, immunoassays and other such applications. The matrix herein can be particulate or can be in the form of a continuous surface, such as a microtiter dish or well, a glass slide, a silicon chip, a nitrocellulose sheet, nylon mesh, or other such materials. When particulate, typically the particles have at least one dimension in the 5-10 mm range or smaller. Such particles, referred collectively herein as "beads", are often, but not necessarily, spherical. Such reference, however, does not constrain the geometry of the matrix, which may be any shape, including random shapes, needles, fibers, and elongated. Roughly spherical "beads", particularly microspheres that can be used in the liquid phase, are also contemplated. The "beads" may include additional components, such as magnetic or paramagnetic particles (see, e.g.,, Dyna beads (Dynal, Oslo, Norway)) for separation

using magnets, as long as the additional components do not interfere with the methods and analyses herein.

As used herein, matrix or support particles refers to matrix materials that are in the form of discrete particles. The particles have any shape and dimensions, but typically have at least one dimension that is 100 mm or less, 50 mm or less, 10 mm or less, 1 mm or less, 100  $\mu$ m or less, 50  $\mu$ m or less and typically have a size that is 100 mm<sup>3</sup> or less, 50 mm<sup>3</sup> or less, 10 mm<sup>3</sup> or less, and 1 mm<sup>3</sup> or less, 100  $\mu$ m<sup>3</sup> or less and may be order of cubic microns. Such particles are collectively called "beads."

As used herein, the abbreviations for any protective groups, amino acids and other compounds, are, unless indicated otherwise, in accord with their common usage, recognized abbreviations, or the IUPAC-IUB Commission on Biochemical Nomenclature (see, (1972) *Biochem.* 11:942-944).

## 15 B. DIRECTED EVOLUTION OF A VIRAL GENE

Recombinant viruses have been developed for use as gene therapy vectors. Gene therapy applications are hampered by the need for development of vectors with traits optimized for this application. The high throughput methods provided herein are ideally suited for development of such vectors. In addition to use for development of recombinant viral vectors for gene therapy, these methods can also be used to study and modify the viral vector backbone architecture, transcomplementing helper functions, where appropriate, regulatable and tissue specific promoters and transgene and genomic sequence analyses. Recombinant AAV (rAAV) is a gene therapy vector that can serve these and other purposes.

The rep protein is an adeno-associated virus protein involved in a number of biological processes necessary to AAV replication. The production of the rRep proteins enables viral DNA to replicate,

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encapsulate and integrate (McCarty et al. (1992) J. Virol 66:4050-4057; Horer et al. (1995) J. Virol 69:5485-5496, Berns et al. (1996) Biology of Adeno-associated virus, in Adeno-associated virus (AAV) Vectors in Gene Therapy, K.I. Berns and C. Giraud, Springer (1996); and Chiorini et al. (1996) The Roles of AAV Rep Proteins in gene Expression and Targeted Integration, from Adeno-associated virus (AAV) Vectors in Gene Therapy, K.I. Berns and C. Giraud, Springer (1996)). A rep protein with improved activity could lead to increased amounts of virus progeny thus allowing higher productivity of rAAV vectors.

Since the Rep protein is involved in replication it can serve as a target for increasing viral production. Since it has a variety of functions and its role in replication is complex, it has heretofore been difficult to identify mutations that result in increase viral production. The methods herein, which rely on in vivo screening methods, permit optimization of its activities as assessed by increases in viral production. Provided herein are Rep proteins and viruses and viral vectors containing the mutated Rep proteins that provide such increase. The amino acid positions on the rep proteins that are relevant for rep proteins activities in terms of AAV or rAAV virus production are provided. Those amino acid positions are such that a change in the amino acid leads to a change in protein activity either to lower activity or increase activity. As shown herein, the alanine or amino acid scan revealed the amino acid positions important for such activity (i.e. hits). Subsequent mutations produced by systematically replacing the amino acids at the hit positions with the remaining 18 amino acids produced so-called "leads" that have amino acid changes and result in higher virus production. In this particular example, the method used included the following specific steps.

Amino acid scan

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In order to first identify those amino acid (aa) positions on the rep protein that are involved in rep protein activity, an Ala-scan was performed on the rep sequence. For this, each as in the rep protein sequence was individually changed to Alanine. Any other amino acid, particularly another amino acid such as Gly or Ser that has a neutral effect on structure, could have been used. Each resulting mutant rep protein was then expressed and the amount of virus it produced was measured. The relative activity of each individual mutant compared to the native protein is indicated in FIG 2A. HITS are those mutants that produce a decrease in the activity of the protein (in the example: all the mutants with activities below about 20 % of the native activity).

In a second experimental round, which included a new set of mutations and phenotypic analysis, each amino acid position hit by the Ala-scan step, was mutated by amino acid replacement of the native amino acid by the remaining 18 amino acids, using site-directed mutagenesis.

In both rounds, each mutant was individually designed, generated and processed separately, and optionally in parallel with the other mutants. Neither combinatorial generation of mutants nor mixtures thereof were used in any step of the method.

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A plasmid library was thus generated in which each plasmid contained a different mutant bearing a different amino acid at a different hit position. Again, each resulting mutant rep protein was then expressed and the amount of virus it could produce measured as indicated below. The relative activity of each individual mutant compared to the native protein is indicated in FIGURE 2B. LEADS are those mutants that lead to an increase in the activity of the protein (in the example: the ten mutants with activities higher, typically between 2 to 10 times or more, generally 6-10 time, than the native activity).

#### Expression of the genetic variants and phenotypic characterization.

The rep protein acts as an intracellular protein through complex interaction with a molecular network composed by cellular proteins, DNA, AAV proteins and adenoviral proteins (note: some adenovirus proteins have to be present for the rep protein to work). The final outcome of the rep protein activity is the virus offspring composed by infectious rAAV particles. It can be expected that the activity of rep mutants would affect the titer of the rAAV virus coming out of the cells.

As the phenotypic characterization of the rep variants can only be accomplished by assaying its activity from inside mammalian cells, a mammalian cell-based expression system as well as a mammalian cell-based assay was used. The individual rep protein variants were expressed in human 293 HEK cells, by transfection of the individual plasmids constituting the diverse plasmid library. All necessary functions were provided as follows:

- (a) the cellular proteins present in the permissive specific 293 HEK cells;
- (b) the AAV necessary proteins and DNA were provided by cotransfection of the AAV cap gene as well as a rAAV plasmid vector providing the necessary signaling and substrate ITRs sequences;
- (c) the adenovirus (AV) proteins were provided by co-transfection with a plasmid expressing all the AV helper functions.

A library of recombinant viruses with mutant rep encoding genes was generated. Each recombinant, upon introduction into a mammalian cell and expression resulted in production of rAAV infectious particles. The number of infectious particles produced by each recombinant was determined in order to assess the activity of the rep variant that had generated that amount of infectious particles.

The number of infectious particles produced was determined in a cell-based assay in which the activity of a reporter gene, in the exemplified embodiment, the bacterial lacZ gene, or virus replication (Real time PCR) was performed to quantitatively assess the number of viruses. The limiting dilution (titer) for each virus preparation (each coming from a different rep variant) was determined by serial dilution of the viruses produced, followed by infection of appropriate cells (293 HEK or HeLa rep/cap 32 cells) with each dilution for each virus and then by measurement of the activity of the reporter gene for each dilution of each virus. Hill plots (NAUTSCAN") (published as International PCT application No. WO 01/44809 based on PCT no PCT/FR00/03503, Dec, 2000; see EXAMPLES) or a second order polynomial function (Drittanti et al. (2000) Gene Ther. 7: 924-929; see co-pending U.S. provisional application Serial 60/315,382) was used to analyze the readout data and to calculate the virus titers. Briefly, the titer was calculated from the second order polynomial function by non-linear regression fitting of the experimental data. The point where the polynomial curve reaches its minimum is considered to be the titer of the rAAV preparation. Results are shown in the EXAMPLE below.

Comparison between results of full-length Hit position analysis reporter here and the literature

The experiments identified a number of heretofore unknown mutation loci, which include the hits at positions: 4, 20, 22, 28, 32, 38, 39, 54, 59, 124, 125, 127, 132, 140, 161, 163, 193, 196, 197, 221, 228, 231, 234, 258, 260, 263, 264, 334, 335, 341, 342, 347, 350, 354, 363, 364, 367, 370, 376, 381, 389, 407, 411, 414, 420, 421, 422, 428, 429, 438, 440, 451, 460, 462, 484, 488, 495, 497, 498, 499, 503, 511, 512, 516, 517 and 518 with reference to the amino acids in Rep78 and Rep 68. Rep 78 is encoded by nucleotides 321-

2,186; Rep 68 is encoded by nucleotides 321-1906 and 2228-2252; Rep 52 is encoded by nucleotides 993-2186, and Rep 40 is encoded by amino acids 993-1906 and 2228-2252 of wildtype AAV.

Also among these are mutations that may have multiple effects. Since the Rep coding region is quite complex, some of the mutations have several effects. Amino acids 542, 598, 600 and 601, which are in the to the Rep 68 and 40 intron region, are also in the coding region of Rep 78 and 52. Codon 630 is in the coding region of Rep 68 and 40 and non coding region of Rep 78 and 52.

Mutations at 10, 86, 101, 334 and 519 have been previously identified, and mutations, at loci 64, 74, 88, 175, 237, 250 and 429, but with different amino acid substitutions, have been previously reported. In all instances, however, the known mutations reportedly decrease the activity of Rep proteins. Among mutations described herein, are mutations that result in increases in the activity the Rep function as assessed by detecting increased AAV production.

In particular, as described in the Example, mutations in the Repenceding region of AAV, including serotypes AAV-1, AAV-2, AAV-3, AAV-3B, AAV-4, AAV-5 and AAV-6 are provided (see Example below).

- 20 The mutant proteins and mutant adeno-associate virus (AAV) Rep proteins are provided. Exemplary proteins with mutations at one or more of residues 4, 20, 22, 29, 32, 38, 39, 54, 59, 124, 125, 127, 132, 140, 161, 163, 193, 196, 197, 221, 228, 231, 234, 258, 260, 263, 264, 334, 335, 337, 342, 347, 350, 354, 363, 364, 367, 370, 376, 381,
- 389, 407, 411, 414, 420, 421, 422, 424, 428, 438, 440, 451, 460, 462, 484, 488, 495, 497, 498, 499, 503, 511, 512, 516, 517, 518, 542, 548, 598, 600 and 601 of AAV-2 or the corresponding residues in other serotypes are provided. Residue 1 corresponds to residue 1 of the Rep78 protein encoded by nucleotides 321-323 of the AAV-2 genome

(see Figure 3 and the Table below for an alignment of the mutations from various serotypes).

Of particular interest are mutations that increase activity of the Rep proteins compared to wildtype. Such mutations include one or more of residues 350, 462, 497, 517, 542, 548, 598, 600 and 630 of AAV-2 and the corresponding residues in other serotypes. Also provided are mutations at or near those residues, such as within about 1 to about 10 residues of these residues such that the resulting protein has increased activity. Mutations include insertions, deletions and replacements.

### 10 Lead identification.

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Based on the results obtained from the assays described herein (i.e. titer of virus produced by each rep variant), each individual rep variant was assigned a specific activity. Those variant proteins displaying the highest titers were selected as leads and are used to produce rAAV.

In further steps, rAAV and Rep proteins that contain a plurality of mutations based on the hits (see Table in the EXAMPLE, listing the hits and lead sites), are produced to produce rAAV and Rep proteins that have activity that is further optimized. Examples of such proteins and AAV containing such proteins are described in the EXAMPLE. Other combinations of mutations can be prepared and tested as described herein to identify other leads of interest, particularly those that have increased Rep protein activity or that result in higher viral titers in cells containing such viruses that include appropriate *cis* acting elements for viral production.

The rAAV rep mutants are used as expression vectors, which, for example, can be used transiently for the production of recombinant AAV stocks. Alternatively, the recombinant plasmids may be used to generate stable packaging cell lines.

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Also among the uses of rAAV, particularly the high titer stocks produced herein, is gene therapy for the purpose of transferring genetic information into appropriate host cells for the management and correction of human diseases including inherited and acquired disorders such as cancer and AIDS. The rAAV can be administered to a patient at therapeutically effective doses.

# C. Uses of the mutant Rep genes and the rAAV Gene therapy

The rAAV provided herein are intended for use as vectors for gene therapy. The rAAV provided herein are intended for use in any gene therapy protocol the uses AAV as a vector. The mutant Rep proteins and nucleic acid molecules can be used to replace the corresponding gene in other AAV vectors. Of interest are the mutations provided herein that increase rAAV production. In particular, the mutant Rep proteins are used to increase production of rAAV derived from any of the AAV serotypes, including AAV-1, AAV-2, AAV-3, AAV-3B, AAV-4, AAV-5 and AAV-6 serotypes.

Toxicity and therapeutic efficacy of the rAAV can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the LDS $_{50}$  (the dose lethal to 50% of the population) and the ED50 (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio LD $_{50}$ /ED $_{50}$ . Doses that exhibit large therapeutic indices are preferred. Doses that exhibit toxic side effects may be used; care should be taken to design a delivery system that targets rAAV to the site of treatment in order to minimize damage to untreated cells and reduce side effects.

The data obtained from cell culture assays and animal studies can be used in formulating a range of dosage for use in humans. The dosage of such rAAV lies preferably within a range of circulating concentrations that include the ED<sub>50</sub> with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. A therapeutically effective dose can be estimated initially from cell culture assays. A dose may be formulated in animal models to achieve a circulating plasma concentration range that includes the IC<sub>50</sub> (ie., the concentration of the test compound which achieves a half-maximal infection or a half- maximal inhibition) as determined in cell culture. Such information can be used to more accurately determine useful doses in humans. Levels in plasma may be measured, for example, by high performance liquid chromatography.

Treatment of Cancer, HIV, and papilloma and herpes virus infections and diseases mediated thereby

AAV, which is a helper-dependent parvovirus requires co-infection with an adenovirus, herpes virus or papilloma virus (PV) for replication and particle formation. AAV inhibits PV-induced oncogenic tansformation, and this inhibition has been mapped to the Rep78 protein. The Rep78 protein inhibits expression of the PV promoter just upstream of the E6 gene (p89 of bovine PV-1 (BPV-1)) p97 of human PV-16 (HPV-16), and p105 of human PV-18 (HPV-18)). DNA binding is required for this inhibition. Rep78 also binds to the TAR sequences (nt +23 to +42) and to a region just upstream of the TATA box (nt. -54 to -34) in the HIV LTR region. AAV Rep78 also regulates a variety of other cancer associated genes, including, but are not limited to, C-H-ras (Khleif et al. (1991) Virology 181:738-741), c-fos and c-myc (Hermonat (1994) Cancer Lttrs 81:129-136).

Infection by AAV is negatively associated with cervical cancer. Infection and DNA integration by certain PV types are central events in the etiology of cervical cancer (Durst et al. (1983) Proc. Natl. Acad. Sci.

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U.S.A. 80:3812-3815; Cullen et al. (1991) J. Virol. 65:606-612). Roughly two thirds of cervical cancers contain the HPV-16 virus. AAV is also commonly found in the anogenital region (Han et al. (1996) Virus Genes 12:47-52.

5 Contemplated herein are AAV rep mutants that bind with greater affinity than wild-type AAV Rep78 to nucleic acid from PV, AAV, oncogenes or HIV, particularly HIV-1, and particularly promoter and other transcriptional/translational regulatory sequences from these sources. The mutant Rep protein when administered to a subject can inhibit PV and PV-associated diseases, HIV and HIV-associated diseases. Hence methods for treatment of PV and HIV-mediated disorders by administration of rAAV encoding mutant the Rep78 genes are provided. The particular mutants for use in these methods can be identified by testing each mutant for inhibitory activity, for example, in cell-based assays. For example, the Rep mutant protein can be tested by contacting it with nucleic acid from a PV, AAV or HIV or oncogene for a time sufficient to permit binding thereto, and comparing such binding to the binding of a wild-type Rep protein under the same conditions. Alternatively competitive binding assays may be performed. Mutant proteins having higher binding affinities are identified.

Fusion proteins containing a tat protein of HIV or other targeting agent and mutant Rep protein are also provided. Pharmaceutical compositions containing such fusion proteins are provided. The fusion proteins can contain additional components, such as E. coli maltose binding protein (MBP) that aid in uptake of the protein by cells (see, International PCT application No. WO 01/32711). Nucleic acid molecules encoding the mutant Rep protein or fusion protein operably linked to a promoter, such as an inducible promoter for expression in mammalian cells are also provided. Such promoters include, but are not limited to, CMV and SV40 promoters; adenovirus promoters, such as the E2 gene promoter, which is responsive to the HPV E7 oncoprotein; a PV promoter, such as the PBV p89 promoter that is responsive to the PV E2 protein; and other promoters that are activated by the HIV or PV or oncogenes.

The mutant rep proteins are also delivered to the cells in rAAV or a portion thereof that can additionally encode therapeutic agents for treatment of the cancer or HIV infection or other disorders.

Methods of inhibiting oncogenic transformation by bovine PV (BPV) and by human PV (HPV) are provided.

Methods of inhibiting PV, PV-associated diseases, HIV and HIV-associated diseases are provided. These methods are practiced by administering the proteins, nucleic acids or rAAV or portions thereof to a subject, such as a mammal, including a human to thereby inhibit or modulate disease progression or oncogenic transformation.

### Other systems

It has been shown that the Rep protein is involved in the regulation of gene expression, including viral replication as described above, cellular pathways and protein phosphorylation (see, e.g., Chiorini et al. (1998)

20 Mol. Cell Biol. 18:5921-5929). Hence the mutant Rep proteins provided herein can be used to block, stimulate, inhibit, regulate or otherwise modulate metabolic or cellular signaling pathways. Rep proteins provided herein can be used to block, stimulate, inhibit, regulate or otherwise modulate cyclic AMP response pathways, and also to regulate or modulate cellular promoters as a means of modulating gene expression. Methods using these proteins for such purposes are provided herein.

#### Formulation of rAAV

Pharmaceutical compositions containing the rAAV, fusion proteins or encoding nucleic acid molecules can be formulated in any conventional

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manner by mixing a selected amount of rAAV with one or more physiologically acceptable carriers or excipients. For example, the rAAV may be suspended in a carrier such as PBS (phosphate buffered saline). The active compounds can be administered by any appropriate route, for example, orally, parenterally, intravenously, intradermally, subcutaneously, or topically, in liquid, semi-liquid or solid form and are formulated in a manner suitable for each route of administration. Preferred modes of administration include oral and parenteral modes of administration.

The rAAV and physiologically acceptable salts and solvates may be formulated for administration by inhalation or insufflation (either through the mouth or the nose) or for oral, buccal, parenteral or rectal administration. For administration by inhalation, the rAAV can be delivered in the form of an aerosol spray presentation from pressurized packs or a nebulizer, with the use of a suitable propellant, e.g. dichlorodifluoromethane, trichlorofluoromethane, dichlorotetra-fluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges, e.g. of gelatin, for use in an inhaler or insufflator may be formulated containing a powder mix of a therapeutic compound and a suitable powder base such as lactose or starch.

For oral administration, the pharmaceutical compositions may take the form of, for example, tablets or capsules prepared by conventional means with pharmaceutically acceptable excipients such as binding agents (e.g., pregelatinized maize starch, polyvinylpyrrolidone or hydroxypropyl methylcellulose); fillers (e.g., lactose, microcrystalline cellulose or calcium hydrogen phosphate); lubricants (e.g. magnesium stearate, talc or silica); disintegrants (e.g. potato starch or sodium starch

glycolate); or wetting agents (e.g. sodium lauryl sulphate). The tablets may be coated by methods well known in the art. Liquid preparations for oral administration may take the form of, for example, solutions, syrups or suspensions, or they may be presented as a dry product for constitution with water or other suitable vehicle before use. Such liquid preparations may be prepared by conventional means with pharmaceutically acceptable additives such as suspending agents (e.g. sorbitol syrup, cellulose derivatives or hydrogenated edible fats); emulsifying agents (e.g. lecithin or acacia); non-aqueous vehicles (e.g. almond oil, oily esters, ethyl alcohol or fractionated vegetable oils); and preservatives (e.g. methyl or propyl-p-hydroxybenzoates or sorbic acid). The preparations may also contain buffer salts, flavoring, coloring and sweetening agents as appropriate.

Preparations for oral administration may be suitably formulated to give controlled release of the active compound. For buccal administration the compositions may take the form of tablets or lozenges formulated in conventional manner.

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The rAAV may be formulated for parenteral administration by injection e.g. by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form e.g. in ampoules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents. Alternatively, the active ingredient may be in powder lyophilized form for constitution with a suitable vehicle, e.g., sterile pyrogen-free water, before use.

In addition to the formulations described previously, the rAAV may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example, subcutaneously or

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intramuscularly) or by intramuscular injection. Thus, for example, the therapeutic compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

The active agents may be formulated for local or topical application, such as for topical application to the skin and mucous membranes, such as in the eye, in the form of gels, creams, and lotions and for application to the eye or for intracisternal or intraspinal application. Such solutions, particularly those intended for ophthalmic use, may be formulated as 0.01% - 10% isotonic solutions, pH about 5-7, with appropriate salts. The compounds may be formulated as aerosols for topical application, such as by inhalation (see, e.g., U.S. Patent Nos. 4,044,126, 4,414,209, and 4,364,923, which describe aerosols for delivery of a steroid useful for treatment inflammatory diseases, particularly asthma).

The concentration of active compound in the drug composition will depend on absorption, inactivation and excretion rates of the active compound, the dosage schedule, and amount administered as well as other factors known to those of skill in the art. For example, the amount that is delivered is sufficient to treat the symptoms of hypertension.

The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration.

The active agents may be packaged as articles of manufacture containing packaging material, an agent provided herein, and a label that indicates the disorder for which the agent is provided.

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The following example is included for illustrative purposes only and is not intended to limit the scope of the invention. The specific methods exemplified can be practiced with other species. The examples are intended to exemplify generic processes.

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#### **EXAMPLE**

#### Materials and Methods

#### Cells:

293 human embryo kidney (HEK) cells, obtained from ATCC, were cultured in Dulbecco's modified Eagle's medium containing 4.5 g/l glucose (DMEM; GIBGO-BRL) 10 % fetal bovine serum (FBS, Hyclone). Hela rep-cap 32 cells, described above, were obtained from Anna Salvetti (CHU, Nantes) and cultured in the medium described above.

#### Plasmids:

pNB-Adeno, which encodes the entire E2A and E4 regions and VA
RNA I and II genes of Adenovirus type 5, was constructed by ligating into
the polylinker of multiple cloning site of pBSII KS (+/-) (Stratagene, San
Diego, USA) the Sall-HindIII fragment (9842-11555 nt) of Adenovirus
type 5) and the BamHI-Clal fragment (21563- 35950) of pBR325. All
fragments of adenovirus gene were obtained from the plasmid pBHG-10
(Microbix, Ontario, Canada). pNB-AAV encodes the genes rep and cap of
AAV-2 and was constructed by ligation of Xbal-Xbal PCR fragment
containing the genome of AAV-2 from nucleotide 200 to 4480 into Xbal
site of polylinker MCS of pBSIIKS(+/-). The PCR fragment was obtained
from pAV1 (ATCC, USA). Plasmid pNB-AAV was derived from plasmid
pVA1I, which contains the AAV genomic region, rep and cap. pNB-AAV
does not contain the AAV ITR's present in pAV1. pAAV-CMV(nls)LacZ
was provided by Dr Anna Salvetti (CHU, Nantes).

Plasmid pCMV(nls)LacZ (rAAV vector plasmid) and pNB-Adeno were prepared in DH5a E.coli and purified by Nucleobond AX PC500 Kit

(Macherey-Nagel), according to standard procedures. Plasmid pAAV-CMV(nls)LacZ is derived from plasmid psub201 by deleting the rep-cap region with SnaB I and replacing it with an expression cassette harboring the cytomegalovirus (CMV) immediate early promoter (407 bp), the
nuclear localized β-galactosidase gene and the bovine growth hormone polyA signal (324 bp) (see, Chadeuf et al. (2000) J. Gene Med. 2:260-268. pAAV-CMV(nls)LacZ was provided by Dr Anna Salvetti.

#### Virus:

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Wild type adenovirus (AV) type 5 stock, originally provided by Dr 10 Philippe Moullier (CHU, Nantes), was produced accordingly to standard procedures.

#### Construction of Rep mutant libraries

25 pmol of each mutagenic primer was placed into a 96 PCR well plate. 15  $\mu$ l of reaction mix (0.25 pmol of pNB-AAV), 25 pmol of the selection primer (changing one non-essential unique restriction site to a new restriction site), 2  $\mu$ l of 10X mutagenesis buffer (100mM Tris-acetate pH7.5, 100 mM MgOAc and 500 mM KOAc pH7.5) was added into each well. The samples were incubated at 98 °C for 5 minutes and then immediately incubated for 5 minutes on ice. Finally, the plate was placed at room temperature for 30 minutes.

The primer extension and ligation reactions of the new strands were completed by adding to each sample:  $7 \mu l$  of nucleotide mix (2.86 mM each nucleotide and 1.43 X mutagenesis buffer) and  $3\mu l$  of a fresh 1:10 enzyme dilution mix (0.025U/ $\mu l$  of native T7 DNA polymerase and  $1U/\mu l$  of T4 DNA ligase were diluted in 20mM Tris HCl pH7.5, 10 mM KCl, 10 mM  $\beta$ - mercaptoethanol, 1 mM DTT, 0.1 mM EDTA and 50% glycerol). Samples were incubated at 37°C for 1 hour. The T4 DNA ligase was inactivated by incubating the reactions at 72°C for 15 minutes to

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prevent re-ligation of the digested strands during the digestion of the parental plasmid (pNB-AAV).

Each mutagenesis reaction was digested with restriction enzyme to eliminate parental plasmids: 30  $\mu$ l solution containing 3 $\mu$ l of 10X enzyme digestion buffer and 10 units of restriction enzyme were added to each mutagenesis reaction and incubated at 37°C for at least 3 hours.

90  $\mu$ l of the *E. coli* XLmutS competent cells (Stratagene, San Diego CA; supplemented with 1.5  $\mu$ l of  $\beta$ -mercaptoethanol to a final concentration of 25 mM) were aliquoted into prechilled deep-well plates. The plates were incubated on ice for 10 minutes and swirling gently every 2 minutes.

A fraction of the reactions that had been digested with restriction enzyme (1/10 of the total volume) was added to the deep well plates. The plates were swirled gently prior to incubation on ice for 30 minutes. A heat pulse was performed in a 42°C water bath for 45 seconds, the transformation mixture was incubated on ice for 2 minutes and 0.45 ml of preheated SOC medium (2% (w/v) tryptone, 0.5% (w/v) yeast extract, 8.5 mM NaCl, 2.5 mM KCl, 10 mM MgCl<sub>2</sub> and 20 mM glucose at pH 7) was added. The plates were incubated at 37°C for 1 hour with shaking.

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To enrich for mutant plasmids, 1 ml of 2X YT broth medium (YT medium is 0.5% yeast extract, 0.5% NaCl, 0.8% bacto-tryptone), supplemented with 100  $\mu$ g/ml of ampicillin, was added to each transformation mixture and the cultures were grown overnight at 37°C with shaking. Plasmid DNA isolation was performed from each mutant culture using standard procedure described in Nucleospin Multi-96 Plus Plasmid Kit (Macherey-Nagel). Five hundred  $\mu$ g of the resulting isolated DNA was digested with 10 units of the selection restriction enzyme in a total volume of 30 $\mu$ l containing 3  $\mu$ l of 10X enzyme digestion buffer for overnight at 37°C.

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A fraction of the digested reactions (1/10 of the total volume) were transformed into 40  $\mu$ l of Epicurian coli XL1-Blue competent cells supplemented with 0.68  $\mu$ l of  $\beta$ -mercaptoethanol to a final concentration of 25 mM. After heat pulse, 0.45 ml of SOC was added and the transformation mixtures were incubated for 1 hour at 37°C with shaking before to be plate on LB-ampicillin agar plates. The agar plates were incubated overnight at 37°C and the colonies obtained were picked up and grown overnight at 37°C into deep-well plates.

Four clones per reaction were screened for the presence of the mutation using restriction enzyme specific to the new restriction site introduced into the mutated plasmid with the selection primer. The cDNA from selected clones was also sequenced to confirm the presence of the expected mutation.

#### **Monitoring rAAV Production**

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15 rAAV from each of the above wells, were produced by triple transfection on 293 HEK cells. 3 x 104 cells were seeded into each well of 96 micro-well plate and cultured for 24 hours before transfection. Transfection was made on cells at about 70% confluency. 25 kDa PEI (poly-ethylene-imine, Sigma-Aldrich) was used for the triple transfection step. Equimolar amounts of the three plasmids AV helper plasmid (pNB-Adeno), AAV helper plasmid (pNB-AAV or a mutant clone rep plasmid) and vector plasmid (pAAV-CMV(nls)LacZ) were mixed with 10 mM PEI by gently shaking. The mixture was the added to the medium culture on the cells. 60 hours after transfection, the culture medium was replaced with 25 100  $\mu$ l of lysis buffer (50mM Hepes, pH 7.4; 150 mM NaCl; 1mM MgCl<sub>2</sub>; 1 mM CaCl<sub>2</sub>; 0.01% CHAPS). After one cycle of freeze-thawing the cellular lysate was filtered through a millipore filter 96 well plate and stored at -80°C.

#### rAAV infection particles (ip)

Titers of rAAV vector particles were determined on HeLa rep/cap 32 cells using standard dRA (serial dilution replication assay) test. Cells were plated 24 hours before infection at a density of 1 x 10<sup>4</sup> cells in 96-well plates. Serial dilutions of the rAAV preparation were made between 1 and 1 x 10<sup>6</sup> µl and used for co-infection of the HeLa rep/cap 32 cells together with wt-AV type 5 (MOI 25). 48 hours after infection the ip were measured by real time PCR or by the quantification of biological activity of the transgene.

#### 10 Real Time PCR

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Infected HeLa rep/cap 32 cells were lysed with 50  $\mu$ l of solution (50 mM Hepes, pH 7.4; 150 mM NaCl). After one cycle of freeze-thawing 50  $\mu$ l of Proteinase K (10 mg/ml) and the lysate were incubated one hour at 55 °C. The enzyme was inactivated by incubation 10 min at 96 °C.

For real time PCR, 0.2 μl of lysate was taken. Final volume of the reaction was 10 μl in 384 well plate using an Applied Biosystem Prism 7900. The primers and fluorescence probe set corresponding to the CMV promoter were as follows: CMV 1 primer 5'-

TGCCAAGTACGCCCCCTAT-3' (SEQ ID No. 733) (0.2  $\mu$ M) and CMV 2 primer 5'-AGGTCATGTACTGGGCATAATGC -3' (SEQ ID No. 734) (0.2  $\mu$ M); probe VIC-Tamra 5'-TCAATGACGGTAAATGGCCCGCCT-3' (SEQ ID No. 735) (0.1  $\mu$ M). dRA plots were obtained by plotting the DNA copy number (obtained by real time PCR) vs. the dilution of the rAAV preparation.

## $\beta$ -Galactosidase activity

After 48 hours of infection, cells were treated with trypsin, and  $100~\mu l$  of reaction solution (GalScreen Kit, Tropix) was added and incubated for one hour at 26 °C. Luminescence was measured in NorthStar (Tropix) HTS station. dRA plots were obtained plotting the

intensity of  $\beta$ -Galatosidase activity vs. the dilution of the rAAV preparation.

# Mathematical Model for results analysis:

Results were analyzed using the Hill equation-based analysis

(designated NautScan<sup>TM</sup>; see, Patent n° 9915884, 1999, France;
published as International PCT application No. WO 01/44809 (PCT n° PCT/FR00/03503, Dec, 2000). Briefly, data were processed using a Hill equation-based model that allows extraction of key feature indicators of performance for each individual mutant. Mutants were ranked based on the values of their individual performance and those at the top of the ranking list were selected as Leads.

#### Results

#### Generation of diversity.

To identify candidate amino acid (aa) positions on the rep protein involved in rep protein activity an Ala-scan was performed on the rep sequence. For this, each amino acid in the rep protein sequence was replaced with Alanine. To do this sets of rAAV that encode mutant rep proteins in which each differs from wild type by replacement of one amino acid with Ala, were generated. Each set of rAAV was individually introduced into cells in a well of a microtiter plate, under conditions for 20 expression of the rep protein. The amount of virus that could be produced from each variant was measured as described below. Briefly, activity of Rep was assessed by determining the amount of AAV or rAAV produced using infection assays on HeLa Rep-cap 32 cells and by measurement of AAV DNA replication using Real Time PCR, or by assessing transgene (eta-galactosidase) expression. The relative activity of each individual mutant compared to the native protein was assessed and "hits" identified. Hit positions are the positions in the mutant proteins that resulted in an alteration (selected to be at least about 20%), in this

instance all resulted in a decrease, in the amount of virus produced compared to the activity of the native (wildtype) gene (see Fig. 2A).

The hits were then used for identification of leads (see, Fig. 2B).

Assays for Rep activity were performed as described for identification of
the hit positions. Hit positions on Rep proteins and the effect of specific
amino acids on the productivity of AAV-2 summarized in the following
table:

	Hit position	replacing amin	o acid (effect)
	4 (ttt) F	(gct) A (decrease)	
10	10 (aag) K	(gcg) A (decrease)	
	20 (ccc) P	(gcc) A (decrease)	
	22 (att) I	(gct) A (decrease)	
	28 (tgg) W	(gcg) A (decrease)	
•	32 (gag) E	(gcg) A (decrease)	
15	38 (ccg) P	(gcg) A (decrease)	·
	39 (cca) P	(gca) A (decrease)	
	54 (ctg) L	(gct) A (decrease)	
	59 (ctg) L	(gcg) A (decrease)	
	64 (ctg) L	(gcg) A (decrease)	
20	74 (ccg) P	(gcg) A (decrease)	
	86 (gag) E	(gcg) A (decrease)	
	88 (tac) Y	(gcc) A (decease)	
.	101 (aaa) K	(gca) A (decrease)	
	124 (atc) I	(gcc) A (decrease)	
25	125 (gag) E	(gcg) A (decrease)	
	127 (act) T	(gct) A (decrease)	
	132 (ttc) F	(gcc) A (decrease)	
	140 (ggc) G	(gcc) A (decrease)	

Hit position replacing amino acid (effect 161 (acc) T (gcc) A (decrease)  163 (cct) P (gct) A (decrease)  175 (tat) Y (gct) A (decrease)  193 (ctg) L (gcg) A (decrease)  196 (gtg) V (gcg) A (decrease)  197 (tcg) S (gcc) A (decrease)  221 (tca) S (gca) A (decrease)  228 (gtc) V (gcg) A (decrease)  231 (ctc) L (gcc) A (decrease)  234 (aag) K (gcg) A (decrease)  237 (acc) T (gcc) A (decrease)  250 (tac) Y (gcc) A (decrease)	t)
163 (cct) P (gct) A (decrease)  175 (tat) Y (gct) A (decrease)  193 (ctg) L (gcg) A (decrease)  196 (gtg) V (gcg) A (decrease)  197 (tcg) S (gcc) A (decrease)  221 (tca) S (gca) A (decrease)  228 (gtc) V (gcg) A (decrease)  231 (ctc) L (gcc) A (decrease)  234 (aag) K (gcg) A (decrease)  237 (acc) T (gcc) A (decrease)	
175 (tat) Y (gct) A (decrease)  193 (ctg) L (gcg) A (decrease)  196 (gtg) V (gcg) A (decrease)  197 (tcg) S (gcc) A (decrease)  221 (tca) S (gca) A (decrease)  228 (gtc) V (gcg) A (decrease)  231 (ctc) L (gcc) A (decrease)  234 (aag) K (gcg) A (decrease)  237 (acc) T (gcc) A (decrease)	
193 (ctg) L (gcg) A (decrease)  196 (gtg) V (gcg) A (decrease)  197 (tcg) S (gcc) A (decrease)  221 (tca) S (gca) A (decrease)  228 (gtc) V (gcg) A (decrease)  231 (ctc) L (gcc) A (decrease)  234 (aag) K (gcg) A (decrease)  237 (acc) T (gcc) A (decrease)	
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231 (ctc) L (gcc) A (decrease) 234 (aag) K (gcg) A (decrease) 237 (acc) T (gcc) A (decrease)	
10 234 (aag) K (gcg) A (decrease) 237 (acc) T (gcc) A (decrease)	
237 (acc) T (gcc) A (decrease)	
250 (tac) Y (gcc) A (decrease)	-
1 <del></del>	
258 (aac) N (gcc) A (decrease)	
260 (cgg) R (gcg) A (decrease)	
15 263 (atc) I (gcc) A (decrease)	
264 (aag) K (gcg) A (decrease)	
334 (ggg) G (gcg) A (decrease)	
335 (cct) V (gct) A (decrease)	_
337 (act) T (gct) A (decrease)	
20 341 (acc) T (gcc) A (decrease)	
342 (aac) N (gcc) A (decrease)	
347 (ata) I (gca) A (decrease)	
350 (act) T (gct) A (decrease (aat) N (incre	ase)
354 (tac) Y (gcc) A (decrease)	
5 363 (aac) N (gcc) A (decrease)	
364 (ttt) F (gct) A (decrease)	

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	Hit position	replacing an	nino acid (effect)
	367 (aac) N	(gcc) A (decrease)	
	370 (gtc) V	(gcc) A (decrease)	
	376 (tgg) W	(gcg) A (decrease)	
	381 (aag) K	(gcg) A (decrease)	
5	382 (atg) M	(gcg) A (decrease)	
	389 (tcg) S	(gcg) A (decrease)	)
	407 (tcc) S	(gcc) A (decrease)	
	411 (ata) I	(gca) A (decrease)	
	414 (act) T	(gct) A (decrease)	
10	420 (tcc) S	(gct) A (decrease)	
	421 (aac) N	(gcc) A (decrease)	
	422 (acc) T	(gcc) A (decrease)	
	424 (atg) M	(gcg) A (decrease)	
	428 (att) I	(gct) A (decrease)	
15	429 (gac) D	(gcc) A (decrease)	
	438 (cag) Q	(gcg) A (decrease)	-
	440 (ccg) P	(gcg) A (decrease)	
	451 (acc) T	(gcc) A (decrease)	
	460 (aag) K	(gcg) A (decrease)	
20	462 (acc) T	(gcc) A (decrease)	(ata) I (increase)
	484 (ttc) F	(gcc) A (decrease)	
	488 (aag) K	(gcg) A (decrease)	·
	495 (ccc) P	(gcc) A (decrease)	
	497 (ccc) P	(gcc) A (decrease)	(cga) R (increase)
5	497 (ccc) P	(gcc) A (decrease)	(ctc) L (increase)
	497 (ccc) P	(gcc) A (decrease)	(tac) Y (increase)

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		<del></del>	<del>`</del>
	Hit position	replacing ami	no acid (effect)
	498 (agt) S	(gct) A (decrease)	
	499 (gac) D	(gcc) A (decrease)	•
	503 (agt) S	(gcg) A (decrease)	
5	511 (tca) S	(gca) A (decrease)	
	512 (gtt) V	(gct) A (decrease)	
	516 (tcg) S	(gcg) A (decrease)	
	517 (acg) T	(gct) A (decrease)	(aac) N (increase)
	518 (tca) S	(gca) A (decrease)	
	519 (gac) D	(gcg) A (decrease)	
10	542 (ctg) L	(gcg) A (decrease)	(tcg) S (increase)
·	548 (aga) R	(gca) A (decrease)	(agc) S (increase)
	598 (gga) G	(gca) A (decrease)	(agc) S (increase)
	600 (gtg) V	(gcg) A (decrease)	(ccg) P (increase)
15	601 (cca) P	(gca) A (decrease)	
	Hit position (within intron)	replacing sequence	(effect)
	630 (tgc)	gcg (decrease)	cgc or tca or cct (increase)

The hits in other AAV serotypes (see, also Figures 3A and 3B) are 20 as follows:

HIT POSITION							
AAV-2	AAV-1	AAV-3	AAV-3B	AAV-4	AAV-6	AAV-5	
4	4	4	4	4	4	4	
10	10	10	10	10	10	10	
20	20	20	20	20	20	20	
22	22	22	22	22	22	22	
29	29	29	29	29	29	29	

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				HIT POSITI	ON		
	32	32	32	32	32	32	32
	38	38	38	38	38	38	38
	39	39	39	39	39	39	39
	54	54	54	54	54	54	54
5	59	59	59	59	59	59	59
	64	64	64	64	64	64	64
	74	74	74	74	74	74	
	86	86	86	86	86	86	85
	88	88	88	88	88	88	87
10	101	101	101	101	101	101	100
	124	124	124	124	124	124	123
	125	125	125	125	125	125	124
	127	127	127	127	127	127	126
•	132	132	132	132	132	132	131
15	140	140	140	140	140	140	
	161	161	161	161	161	161	158
	163	163	163	-163	163	163	160
	175	175	175	175	175	175	172
•	193	193	193	193	193	193	190
20	196	196	196	196	196	196	193
	197	197	197	197	197	197	194
	221	221	221	221	221	221	217
	228	228	228	228	228	228	224
	231	231	231	231	231	231	227
25	234	234	234	234	234	234	230
	237	237	237	237	237	237	233
	250	250	250	250	250	250	246
	258	258	258	258	258	258	254
l	260	260	260	260	260	260	256

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		·						
	HIT POSITION							
	263	263	263	263	263	263	259	
	264	264	264	264	264	264	260	
•	334	334	334	334	334	334	330	
	335	335	335	335	335	335	331	
5	337	. 337	337	337	337	337	333	
	341	341	341	341	341	341	337	
	342	342	342	342	342	342	338	
	347	347	347	347	347	347	342	
	350	350	350	350	350	350	346	
10	354	354	354	354	354	354	350	
	363	363	363	363	363	363	359	
	364	364	364	364	364	364	360	
	367	367	367	367	367	367	363	
	370	370	370	370	370	370	366	
15	376	376	376	376	376	376	372	
	381	381	381	381	381	381	377	
	382	382	382	382	382	382	378	
	389	389	389	389	389	389	385	
	407	407	407	407	407	407	403	
20	411	411	411	411	411	411	407	
	414	414	414	414	414	414	410	
	420	420	420	420	420	420	416	
	421	421	421	421	421	421	417	
	422	422	422	422	422	422	418	
25	424	424	424	424	424	424	420	
	428	428	428	428	428	428	424	
	429	429	429	429	429	429	425	
	438	438	438	438	438	438	434	
[	440	440	440	440	440	440	436	

		HIT POSITION							
	451	451	451	451	451	451	447		
	460	460	460	460	460	460	456		
	462	462	462	462	462	462	458		
	484	484	484	484	484	484	480		
5	488	488	488	488	488	488	484		
	495	495	495	495	495	495	491		
	497	497	497	497	497	497	493		
	498	498	498	498	498	498	494		
	499	499	499	499	499	499	495		
10	503	503	503	503	503	503	499		
	511	511	511	511	511	511	529		
	512	512	512	512	512	512	530		
	516	516	516	516	516	516	534		
	517	517	517	517	517 .	517	535		
15.	518	518	518	518	518	518	536		
	519	519	519	519	519	519	537		
٠	542	543	542	542	542	543	561		
	548	549	54 <b>8</b>	548	548	549	567		
	598	599	600	600	599	599			
20	600	602	603	603	602	602	589		
	601	603	604	604	603	603	590		

Sets of nucleic acids encoding the rep protein were generated. The rep proteins encoded by these sets of nucleic acid molecules were those 25 in which each amino acid position identified as a "hit" in the ala-scan step, were each sequentially replaced by all remaining 18 amino acids using site directed mutagenesis. Each mutant was designed, generated, processed and analyzed physically separated from the others in

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addressable arrays. No mixtures, pools, nor combinatorial processing were used.

As in the first round (alanine scan), a library of mutant rAAV was generated in which each individual mutant was independently and individually generated in a independent reaction and such that each mutant contains only a single amino acid change and this for each amino acid residue. Again, each resulting mutant rep protein was then expressed and the amount of virus produced in cells assessed and compared to the native protein.

#### 10 Lead identification

Since rep proteins that result in increased virus production are of interest, those mutants that lead to an increase in the amount of virus produced (2 to 10 times the native activity), were selected as "leads." Ten such mutants were identified.

Based on the results obtained from the assays described above (i.e. titer of virus produced by each rep variant), each individual rep variant was assigned a specific activity. Those variant proteins displaying the highest titers were selected as leads (see Table above). Leads include: amino acid replacement of T by N at Hit position 350; T by I at Hit position 462; P by R at Hit position 497; P by L at Hit position 497; P by Y at Hit position 497; T by N at Hit position 517; L by S at Hit position 542; R by S at Hit positio 548, G by S at Hit position 598; G by D at Hit position 598; V by P at Hit position 600.

Also provided are combinations of the above mutant Rep 78, 68, 52. 40 proteins, nucleic acids encoding the proteins, and recombinant AAV (any serotype) containing the mutation at the indicated position or corresponding position for serotypes other than AAV-2, including any set forth in the following table and corresponding SEQ ID Nos. Each amino acid sequence is set forth in a separate sequence ID listing; for each

mutation or combination thereof there is a single SEQ ID setting forth the unspliced nucleic acid sequence for Rep78/68, which for all mutations from amino acid 228 on, includes the corresponding Rep 52 and Rep 40 encoding sequence as well.

# 5 Amino acid sequences of exemplary mutant Rep proteins

Seq no. gene position(s)	codon(s)
seq.1 rep78 4	GCT
•	GCT
seq.3 rep78 10	GCG
10	GCG
	GCC
	GCC
	GCT
seq.8 rep68 22 d	GCT
1E	GCG
	GCG
	GCG
. 45	GCG ·
seq.13 rep78 39	GCA ·
	3CA
	3CT
seq.16 rep68 53 G	€T
	GCG
	GCG
	CT
	CT
	CG
	CG
seq.23 rep78 86 G	iCG
	CG
	CC
	CC
	CA
	CA ·
124	CC
	CC
	CG
,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	CG
40	CT
12/	CT
102	CC
27	
45 20	
seq.40 rep68 161 GC	

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	seq.41	rep78	163	, GCT
	seq.42	rep68	163	GCT
	seq.43	rep78	175	GCT
	seq.44	rep68	175	GCT
5	seq.45	rep78	193	GCG
	seq.46	rep68	193	GCG
	seq.47	rep78	196	GCC
	seq.48	rep68	196	GCC
	seq.49	rep78	197	GÇC
10	seq.50	rep68	197	GČC
	seq.51	rep78	221	GCA
	seq.52	rep68	221	GCA
	seq.53	rep78	228	GCG
	seq.54	rep52	228	GCG
15	seq.55	rep68	228	GÇG
	seq.56	rep40	228	GCG
	seq.57	rep78	231	GCC
	seq.58	rep52	231	GCC
	seq.59	rep68	231	GCC
20	seq.60	rep40	231	GCC
	seq.61	rep78	234	GCG
	seq.62	rep52	234	GCG
	seq.63	rep68	234	GCG
	seq.64	rep40	234	GCG
25	seq.65	гер78	237	GCC
	seq.66	rep52	237	GCC
	seq.67	rep68	237	GCC
	seq.68	rep40	237	GCC
	seq.69	rep78	250	GCC
30	seq.70	rep52	250	GCC
	seq.71	rep68	250	GCC
	seq.72	rep40	250	GCC
	seq.73	rep78	258	GCC
	seq.74	rep52	258	GCC
35	seq.75	rep68	258	GCC
	seq.76	rep40	258	GCC
	seq.77	rep78	260	GCG
	seq.78	rep52	260	GCG
	seq.79	rep68	260	GCG
40	seq.80	rep40	260	GCG
	seq.81	rep78	263	GCC
	seq.82	rep52	263	GCC
	seq.83	rep68	263	GCC
	seq.84	rep40	263	GCC
45	seq.85	rep78	264	GCG
	seq.86	rep52	264	GCG
	seq.87	rep68	264	GCG
	seq.88	rep40	264	GCG
_	seq.89	rep78	334	GCG
50	seq.90	rep52	334	GCG
	seq.91	rep68	334	GCG

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			•	
	seq.92	rep40	334	GCG
	seq.93	rep78	335	GCT
	seq.94	rep52	335	GCT
_	seq.95	rep68	335	GCT
5	seq.96	rep40	335	GCT
	seq.97	rep78	337	GCT
	seq.98	rep52	337	GCT
	seq.99	rep68	337	GCT
10	seq.100	rep40	337	GCT
	seq.101	гер78	341	GCC
	seq.102	rep52	341	GCC
	seq.103	гер68	341	GCC
	seq.104	rep40	341	GCC
	seq.105	rep78	342	GCC
15	seq.106	rep52	342	GCC
	seq.107	rep68	342	GCC
	seq.108	rep40	342	GCC
	seq.109	rep78	347	GCA
	seq.110	rep52	347	GCA
20	seq.111	rep68	347	GCA
	seq.112	rep40	347	GCA
	seq.113	rep78	350	AAT
	seq.114	rep52	350	AAT
	seq.115	rep68	350	AAT
25	seq.116	rep40	350	AAT
	seq.117	rep78	350	GCT
	seq.118	rep52	350	GCT
	seq.119	rep68	350	GCT
	seq.120	rep40	350	GCT
30	seq.121	rep78	354	GCC
	seq.122	rep52	354	GCC
	seq.123	rep68	354	GCC
	seq.124	rep40	354	GCC
	seq.125	rep78	363	GCC
35	seq.126	rep52	363	GCC
	seq.127	rep68	363	GCC
	seq.128	rep40	363	GCC
	seq.129	rep78	364	GCT
	seq.130	rep52	364	GCT
40	seq.131	rep68	364	GCT
	seq.132	rep40	364	GCT
	seq.133	rep78	367	GCC
	seq.134	rep52	367	GCC
45	seq.135	rep68	367	GCC
	seq.136	rep40	367	GCC
	seq.137	rep 78	370	GCC
	seq.138	rep52	370	GCC
	seq.139	rep68	370	GCC
	seq.140	rep40	370	GCC
50	seq.141	rep 78	376	GCG
	seq.142	rep52	376	GCG
			5.0	900

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	seq.143	гер68	376	GCG
	seq.144	rep40	376	GCG
	seq.145	rep78	381	GCG
_	seq.146	rep52	381	GCG
5	seq.147	.rep68	381	GCG
	seq.148	rep40	381	GCG
	seq.149	rep78	382	GCG
	seq.150	rep52	382	GCG
	seq.151	rep68	382	GCG
10	seq.152	rep40	382	GCG
	seq.153	rep78	389	GCG
	seq.154	rep52	389	GCG
	seq.155	rep68	389	GCG
	seq.156	rep40	389	GCG
15	seq.157	rep78	407	GCC
	seq.158	rep52	407	GCC
	seq.159	rep68	407	GCC
	seq.160	гер40	407	GCC
	seq.161	rep78	411	GCA
20	seq.162	rep52	411	GCA
	seq.163	rep68	411	GCA
	seq.164	rep40	411	GCA
	seq.165	rep78	414	GCT
	seq.166	rep52	414	GCT
25	seq.167	rep68	414	GCT
	seq.168	rep40	414	GCT
	seq.169	rep78	420	GCT
	seq.170	rep52	420	GCT
	seq.171	rep68	420	GCT
30	seq.172	rep40	420	GCT
	seq.173	rep78	421	GCC
	seq.174	rep52	421	GCC
	seq.175	rep68	421	GCC
	seq.176	rep40	421	GCC
35	seq.177	rep78	422	GCC
	seq.178	rep52	422	GCC
	seq.179	rep68	422	GCC
	seq.180	rep40	422	GCC
	seq.181	rep78	424	GCG
40	seq.182	rep52	424	GCG
	seq.183	гер68	424	GCG
	seq.184	rep40	424	GCG
	seq.185	rep78	428	GCT
	seq.186	rep52	428	GCT
45	seq.187	rep68	428	GCT
	seq.188	rep40	428	GCT
	seq.189	rep78	429	GCC
	seq.190	rep52	429	GCC
	seq.191	rep68	429	GCC
50	seq.192	rep40	429	GCC
	seq.193	rep78	438	GCG
	-	- F · -		000

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	seq.194	rep52	438	GCG
	seq.195	rep68	438	GCG
	seq.196	rep40	438	GCG
	seq.197	rep78	440	GCG
,	5 seq.198	rep52	440	GCG
	seq.199	rep68	440	GCG
	seq.200	гер40	440	GCG
	seq.201	гер78	451	GCC
	seq.202	rep52	451	GCC
10	1	rep68	451	GCC
	seq.204	rep40	451	GCC
	seq.205	rep78	460	GCG
	seq.206	rep52	460	GCG
	seq.207	rep68	460	GCG
15	seq.208	rep40	460	GCG
	seq.209	rep78	462	GCC
	seq.210	rep52	462	GCC
	seq.211	rep68	462	GCC
	seq.212	rep40	462	GCC
20	seq.213	rep78	462	ATA
	seq.214	rep52	462	ATA
	seq.215	rep68	462	ATA
	seq.216	rep40	462	ATA
	seq.217	rep78	484	GCC
25	seq.218	rep52	484	GCC
	seq.219	rep68	484	GCC
	seq.220	rep40	484	GCC
	seq.221	rep78	488	GCG
	seq.222	rep52	488	GCG
30	seq.223	rep68	488	GCG
	seq.224	rep40	488	GCG
	seq.225-	rep78	495	GCC
	seq.226	rep52	495	GCC
	seq.227	rep68	495	GCC
35	seq.228	rep40	495	GCC
	seq.229	rep78	497	GCC
	seq.230	rep52	497	GCC
	seq.231	rep68	497	GCC
	seq.232	rep40	497	GCC
40	. seq.233	rep78	497	CGA
	seq.234	rep52	497	CGA
	seq.235	гер68	497	CGA
	seq.236	rep40	497	CGA
	seq.237	rep78	497	CTC
45	seq.238	rep52	497	CTC
	seq.239	rep68	497	CTC
	seq.240	rep40	497	CTC
	seq.241	rep78	497	TAC
_	seq.242	rep52	497	TAC
50	seq.243	rep68	497	TAC
	seq.244	rep40	497	TAC
		•		170

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			•	
	seq.245	rep78	498	GCT
-	seq.246	rep52	498	GCT
	seq.247	rep68	498	GCT
_	seq.248	rep40	498	GCT
Ę	seq.249	rep78	499	GCC
	seq.250	rep52	499	GCC
	seq.251	гер68	499	GCC
	seq.252	rep40	499	GCC
	seq.253	rep78	503	GCG
10	seq.254	rep52	503	GCG
	seq.255	rep68	503	GCG
•	seq.256	rep40	503	GCG
	seq.257	rep78	510	GCA
4-	seq.258	rep52	510	GCA
15		rep68	510	GCA
	seq.260	rep40	510	GCA
	seq.261	rep78	511	GCA
	seq.262	rep52	511	GCA
20	seq.263	rep68	511	. GCA
20	seq.264	rep40	511	GCA
	seq.265	rep78	512	GCT
	seq.266	rep52	512	GCT
	seq.267	rep68	512	GCT.
25	seq.268	rep40	512	GCT
25	seq.269	rep78	516	GCG
	seq.270	rep52	516	GCG
	seq.271	rep68	516	GCG
	seq.272	rep40	516	GCG
30	seq.273	rep78	517	GCT
30	seq.274	rep52	517	GCT
	seq.275	rep68	517	GCT
	seq.276- seq.277	rep40	517	GCT
	seq.277	гер78	517	AAC
35	seq.279	rep52	. 517	AAC
-00	seq.275	rep68	517	AAC
	seq.281	rep40	517	AAC
	seq.282	rep78 rep52	518 518	GCA
	seq.283	rep68	518 518	GCA
40	seq.284	rep40	518	GCA
	seq.285	rep78	519	GCA
	seq.286	rep52	519	GCG
	seq.287	rep68	519	GCG
	seq.288	rep40	519	GCG
45	seq.289	rep78	598	GCG
	seq.290	rep52	598	GCA GCA
	seq.291	rep78	598	
	seq.292	rep52	598	GAC GAC
	seq.293	rep78	598	AGC
50	seq.294	rep52	598	AGC
	seq.295	rep78	600	GCG
		-		300

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	seq.296	rep52	600	GCG
	seq.297	rep78	600	CCG
	seq.298	rep52	600	CCG
	seq.299	rep78	601	GCA
	<b>5</b> seq.300	rep52	601	GCA
	seq.301	rep78	335 420 495	GCT GCC GCC
	seq.302	rep52	335 420 495	GCT GCC GCC
	seq.303	гер68	335 420 495	GCT GCC GCC
	seq.304	rep40	335 420 495	GCT GCC GCC
1	0 seq.305	rep78	39 140	GCA GCC
	seq.306	rep68	39 140	GCA GCC
	seq.307	rep78	279 428 451	GCC GCT GCC
	seq.308	rep52	279 428 451	GCC GCT GCC
4	_ seq.309	rep68	279 428 451	GCC GCT GCC
1	4.0.0	rep40	279 428 451	GCC GCT GCC
	seq.311	rep78	125 237 600	GCG GCC GCG
	seq.312	rep52	125 237 600	GCG GCC GCG
	seq.313	rep68	125 237 600	GCG GCC GCG
20	seq.314	rep40	125 237 600	GCG GCC GCG
20		rep78	163 259	GCT GCG
	seq.316	rep52	163 259	GCT GCG
	seq.317	rep68	163 259	GCT GCG
	seq.318	rep40	163 259	GCT GCG
25	seq.319	rep78	17 127 189	GCG GCT GCG
20	,	rep68	17 127 189	GCG GCT GCG
	seq.321 seq.322	rep78	350 428	GCT GCT
	seq.322 seq.323	гер52	350 428	GCT GCT
	seq.324	rep68	350 428	GCT GCT
30	seq.325	rep40	350 428	GCT GCT
	seq.326	rep78 rep52	54 338 495	GCC GCC GCC
	seq.327	rep68	54 338 495	GCC GCC GCC
	seq.328	rep40	54 338 495	GCC GCC GCC
	seq.329	rep78	54 338 495	GCC GCC GCC
35	seq.330	rep52	350 420	GCT GCC
	seq.331	rep68	350 420 350 420	GCT GCC
	seq.332	rep40	350 420	GCT GCC
	seq.333	rep78	189 197 518	GCT GCC
	seq.334	rep52	189 197 518	GCG GCG GCA
40	seq.335	rep68	189 197 518	GCG GCG GCA
	seq.336	rep40	189 197 518	GCG GCG GCA
	seq.337	rep78	468 516	GCG GCG GCA GCC GCG
	seq.338	rep52	468 516	GCC GCG
4-	seq.339	rep68	468 516	GCC GCG
45	seq.340	rep40	468 516	GCC GCG
	seq.341	rep78	127 221 350 54 140	GCT GCA GCT GCC GCC
	seq.342	rep52	127 221 350 54 140	GCT GCA GCT GCC GCC
	seq.343	rep68	127 221 350 54 140	GCT GCA GCT GCC GCC
EΛ	seq.344	rep40	127 221 350 54 140	GCT GCA GCT GCC GCC
50	seq.345	rep78	221 285	GCA GCG
	seq.346	rep52	221 285	GCA GCG

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	seq.347	rep68	221 285	GCA GCG
	seq.348	rep40	221 285	GCA GCG
	seq.349	rep78	23 495	GCT GCC
	seq.350	rep52	23 495	GCT GCC
,	5 seq.351	rep68	23 495	GCT GCC
	seq.352	rep40	23 495	GCT GCC
	seq.353	rep78	20 54 420 495	GCC GCC GCC
	seq.354	rep52	20 54 420 495	GCC GCC GCC
	seq.355	rep68	20 54 420 495	GCC GCC GCC
10	. 4	rep40	20 54 420 495	GCC GCC GCC GCC
	seq.357	rep78	412 612	GCC GCG
	seq.358	rep52	412 612	GCC GCG
	seq.359	rep68	412 612	GCC GCG
	seq.360	rep40	412 612	GCC GCG
15	seq.361	rep78	197 412	GCG GCC
	seq.362	rep52	197 412	GCG GCC
	seq.363	rep68	197 412	GCG GCC
	seq.364	rep40	197 412	GCG GCC
	seq.365	rep78	412 495 511	GCC GCC GCA
20	seq.366	rep52	412 495 511	GCC GCC GCA
	seq.367	гер68	412 495 511	GCC GCC GCA
	seq.368	rep40	412 495 511	GCC GCC GCA
	seq.369	rep78	98 422	GCC GCC
	seq.370	rep52	98 422	GCC GCC
25	seq.371	rep68	98 422	GCC GCC
	seq.372	rep40	98 422	GCC GCC
	seq.373	rep78	17 127 189	GCG GCT GCG
	seq.374	rep68	17 127 189	GCG GCT GCG
	seq.375	rep78	20 54 495	GCC GCC GCC
30	seq.376	rep52	20 54 495	GCC GCC GCC
	seq.377	rep68	20 54 495	GCC GCC GCC
	seq.378	гер40	20 54 495	GCC GCC GCC
	seq.379	rep78	259 54	GCG GCC
	seq.380	rep52	259 54	GCG GCC
35	seq.381	rep68	259 54	GCG GCC
	seq.382	rep40	259 54	GCG GCC
	seq.383	rep78	335 399	GCT GCG
	seq.384	rep52	335 399	GCT GCG
40	seq.385	rep68	335 399	GCT GCG
40	seq.386	rep40	335 399	GCT GCG
	seq.387	rep78	221 432	GCA GCA
	seq.388	rep52	221 432	GCA GCA
	seq.389	rep68	221 432	GCA GCA
45	seq.390	rep40	221 432	GCA GCA
45		rep78	259 516	GCG GCG
	seq.392	rep52	259 516	GCG GCG
	seq.393	rep68	259 516 <sub>.</sub>	GCG GCG
	seq.394	rep40	259 516	GCG GCG
50	seq.395	rep78	495 516	GCC GCG
30	seq.396	rep52	495 516	GCC GCG
	seq.397	rep68	495 516	GCC GCG





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	seq.398	rep40	495 516	GCC GCG
	seq.399	rep78	414 14	GCT GCC
	seq.400	rep52	414 14	GCT GCC
_	seq.401	rep68	414 14	GCT GCC
5	seq.402	rep40	414 14	GCT GCC
	seq.403	rep78	74 402 495	GCG GCC GCC
	seq.404	rep52	74 402 495	GCG GCC GCC
	seq.405	rep68	74 402 495	GCG GCC GCC
	seq.406	rep40	74 402 495	GCG GCC GCC
10	seq.407	rep78	228 462 497	GCC GCC GCC
	seq.408	rep52	228 462 497	GCC GCC GCC
	seq.409	rep68	228 462 497	GCC GCC GCC
	seq.410	rep40	228 462 497	GCC GCC GCC
	seq.411	rep78	290 338	GCG GCC
15	seq.412	rep52	290 338	GCG GCC
	seq.413	rep68	290 338	GCG GCC
	seq.414	rep40	290 338	GCG GCC
	seq.415	rep78	140 511	GCC GCA
	seq.416	rep52	140 511	GCC GCA
20	seq.417	rep68	140 511	GCC GCA
	seq.418	rep40	140 511	GCC GCA
*	seq.419	rep78	86 378	GCG GCG
	seq.420	rep52	86 378	GCG GCG
	seq.421	rep68	86 378	GCG GCG
25	seq.422	rep40	86 378	GCG GCG
	seq.423	rep78	54 86	GCC GCG
	seq.424	rep68	54 86	GCC GCG
	seq.425	rep78	54 86	GCC GCG
	seq.426	rep68	54 86	GCC GCG
30	seq.427	rep78	214 495 140	GCG GCC GCC
	seq.428	rep52	214 495 140	GCG GCC GCC
	seq.429	rep68	214 495 140	GCG GCC GCC
	seq.430	rep40	214 495 140	GCG GCC GCC
	seq.431	rep78	495 511	GCC GCA
35	seq.432	rep52	495 511	GCC GCA
	seq.433	rep68	495 511	GCC GCA
	seq.434	rep40	495 511	GCC GCA
	seq.435	rep78	495 54	GCC GCC
	seq.436	rep52	495 54	GCC GCC
40	seq.437	rep68	495 54	GCC GCC
	seq.438	rep40	495 54	GCC GCC
	seq.439	rep78	197 495	GCG GCC
	seq.440	rep52	197 495	GCG GCC
	seq.441	rep68	197 495	
45	seq.442	rep40	197 495	GCG GCC GCG GCC
	seq.443	rep78	261 20	
	seq.444	rep52	261 20	GCC GCC
	seq.445	rep68	261 20	GCC GCC
	seq.446	rep40	261 20	GCC GCC
50	seq.447	rep78	54 20	GCC GCC
- •	seq.448	rep68	54 20 54 20	GCC GCC
		.cpcc	J+ 2U	acc acc

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	seq.449	rep78	197 420	GCG GCC
	seq.450	rep52	197 420	GCG GCC
	seq.451	rep68	197 420	GCG GCC
	seq.452	rep40	197 420	GCG GCC
5	seq.453	rep78	54 338 495	GCC GCC GCC
	seq.454	rep52	54.338 495	GCC GCC GCC
	seq.455	rep68	54 338 495	GCC GCC GCC
	seq.456	rep40	54 338 495	GCC GCC GCC
	seq.457	rep78	197 427	GCG GCG
10	seq.458	rep52	197 427	GCG GCG
	seq.459	rep68	197 427	GCG GCG
	seq.460	rep40	197 427	GCG GCG
	seq.461	rep78	54 228 370 387	GCC GCC GCC GCG
	seq.462	rep52	54 228 370 387	GCC GCC GCC GCG
15	seq.463	rep68	54 228 370 387	GCC GCC GCC GCG
	seq.464	rep40	54 228 370 387	GCC GCC GCC GCG
	seq.465	rep78	221 289	GCA GCC
	seq.466	rep52	221 289	GCA GCC
20	seq.467	rep68	221 289	GCA GCC
20	seq.468	rep40	221 289	GCA GCC
	seq.469	rep78	54 163	GCC GCT
	seq.470	rep68	54 163	GCC GCT
	seq.471	rep78	341 407 420	GCC GCC GCC
25	seq.472	rep52	341 407 420	GCC GCC GCC
25	seq.473	rep68	341 407 420	GCC GCC GCC
	seq.474	rep40	341 407 420	GCC GCC GCC
	seq.475 seq.476	rep78	54 228	GCC GCC
	seq.470 seq.477	rep52	54 228 54 228	GCC GCC
30	seq.478	rep68 rep40	54 228	GCC GCC
00	seq.479	rep40 rep78	54 228 96 125 511	GCC GCC
	seq.480°	rep52	96 125 511	GCA GCG GCA
	seq.481	rep68	96 125 511	GCA GCG GCA
	seq.482	rep40	96 125 511	GCA GCG GCA
35	seq.483	rep78	54 163	GCA GCG GCA GCC GCT
	seq.484	rep68	54 163	GCC GCT
	seq.485	rep78	197 420	GCG GCC
	seq.486	rep52	197 420	GCG GCC
	seq.487	rep68	197 420	GCG GCC
40	seq.488	rep40	197 420	GCG GCC
	seq.489	rep78	334 428 499	GCG GCT GCC
	seq.490	rep52	334 428 499	GCG GCT GCC
	seq.491	rep68	334 428 499	GCG GCT GCC
	seq.492	rep40	334 428 499	GCG GCT GCC
45	sèq.493	гер 78	197 414	GCG GCT
	seq.494	rep52	197 414	GCG GCT
	seq.495	rep68	197 414	GCG GCT
	seq.496	rep40	197 414	GCG GCT
	seq. <b>497</b>	rep78	30 54 127	GCG GCC GCT
50	seq.498	rep68	30 54 127	GCG GCC GCT
	seq.499	rep78	29 260	GCG GCG

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	seq.500	rep52	29 260	GCG GCG
	seq.501	rep68	29 260	GCG GCG
	seq.502	rep40	29 260	GCG GCG
_	seq.503	rep78	4 484	GCT GCC
£	5 seq.504	rep52	4 484	GCT GCC
	seq.505	rep68	4 484	GCT GCC
	seq.506	rep40	4 484	GCT GCC
	seq.507	rep78	258 124 132	GCC GCC GCC
	seq.508	rep52	258 124 132	GCC GCC GCC
10	seq.509	rep68	258 124 132	GCC GCC GCC
	seq.510	rep40	258 124 132	GCC GCC GCC
	seq.511	rep78	231 497	GCC GCC
	seq.512	rep52	231 497	GCC GCC
	seq.513	rep68	231 497	GCC GCC
15	seq.514	rep40	231 497	GCC GCC
	seq.515	rep78	221 258	GCA GCC
	seq.516	rep52	221,258	GCA GCC
	seq.517	rep68	221 258	GCA GCC
	seq.518	rep40	221 258	GCA GCC
20	seq.519	rep78	234 264 326	GCG GCG GCC
	seq.520	rep52	234 264 326	GCG GCG GCC
	seq.521	rep68	234 264 326	GCG GCG GCC
-	seq.522	rep40	234 264 326	
	seq.523	rep78	153 398	GCG GCG GCC
25	seq.524	гер52	153 398	AGC GCG AGC GCG
	seq.525	гер68	153 398	
	seq.526	rep40	153 398	AGC GCG
	seq.527	rep78	53 216	AGC GCG
	seq.528	rep68	53 216	GCG GCC
30	seq.529	rep78	22 382	GCG GCC
	seq.530	rep52	22 382	GCT GCG
	seq.531	rep68	22 382	GCT GCG
	seq.532	rep40	22 382	GCT GCG
	seq.533	rep78	231 411	GCT GCG
35	seq.534	гер52	231 411	GCC GCA
	seq.535	rep68	231 411	GCC GCA
	seq.536	rep40	231 411	GCC GCA
	seq.537	rep78	59 305	GCC GCA
	seq.538	rep52	59 305	GCG GCC
40	seq.539	rep68	59 305	GCG GCC
	seq.540	rep40	59 305	GCG GCC
	seq.541	rep78	53 231	GCG GCC
	seq.542	rep52	53 231	GCG GCC
	seq.543	rep68	53 231	GCG GCC
45	seq.544	rep40	53 231	GCG GCC
	seq.545	rep78	258 498	GCG GCC
	seq.546	rep52	258 498	GCC GCT
	seq.547	rep68	258 498	GCC GCT
	seq.548	rep40	258 498	GCC GCT
50	seq.549	гер78	88 231	GCC GCT
	seq.550	rep52	88 231	GCC GCC
		. 505-	00 23 1	GCC GCC

50

seq.592

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GCC GCC GCA GCC GCA GCC GCA GCC GCA GCC

GCC GCC GCC GCC GCC GCC GCG GCC GCG GCC

	seq.551	rep68	88 231
	seq.552	rep40	88 231
	seq.553	rep78	101 363
	seq.554	rep52	101 363
5	seq.555	rep68	101 363
	seq.556	rep40	101 363
	seq.557	rep78	354 132
	seq.558	rep52	354 132
	seq.559	rep68	354 132
10	seq.560	rep40	354 132
	seq.561	rep78	10 132
	seq.562	rep68	10 132
. • •	DNA Seque	ences	
	Sequence	aa position	codon
15		4	GCT
	seq.564	10	GCG
	seq.565	20	GCC
	seq.566	22	GCT
	seq.567	29	GCG
20	seq.568	38	GCG
	seq.569	39	GCA
	seq.570	53	GCT
	seq.571	59	GCG
	seq.572	64	GCT
25	seq.573	74	GCG
	seq.574	86	GCG
	seq.575	88	GCC
	seq.576	101	GCA
	seq.577	124	GCC
30	seq.578	125	GCG
	seq.579	127	GCT
	seq.580	132	GCC
	seq.581	140	GCC
	seq.582	161	GCC
35	seq.583	163	GCT
	seq.584	175	GCT
	seq.585	193	GCG
	seq.586	196	GCC
	seq.587	197	GCC
40	seq.588	221	GCA
	seq.589	228 (Rep78/68)	GCG
		228 (Rep52)	GCG
		228 (Rep 40)	GCG
4.5	seq.590	231 (Rep78/68)	GCC
45		231 (Rep 52)	GCC
		231 (Rep 40)	GCC
	seq.591	234 (Rep78/68)	GCG
		234 (Rep 52)	GCG
E0		234 (Rep 40)	GCG
50	sea 592	227 (0-20/00)	000

237 (Rep78/68)

GCC

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		. 237 (Rep 52)	GCC
•	seq.593	237 (Rep 40)	GCC
	seq.553	250 (Rep78/68) 250	GCC
5	5	250	GCC
	seq.594	258 (Rep78/68)	GCC
	304.554	258 (nep/6/66)	GCC
		258	GCC
	seq.595	260 (Rep78/68)	GCG
10		260 (1667/8/08)	GCG
		260	GCG
	seq.596	263 (Rep78/68)	GCC
	554.555	263	GCC
		263	GCC
15	seq.597	264 (Rep78/68)	GCG
		264	GCG
		264	GCG
	seq.598	334 (Rep78/68)	GCG
		334	GCG
20		334	GCG
	seq.599	335 (Rep78/68)	GCT
	•	335	GCT
		335	GCT
	seq.600	337 (Rep78/68)	GCT
25		337	GCT
		337	GCT
	seq.601	341 (Rep78/68)	GCC
		341	GCC
00		341	GCC
30	seq.602	342 (Rep78/68)	GCC
	_	342	GCC
		342	GCC
	seq.603	347 (Rep78/68)	GCA
35		347	GCA
33	604	347	GCA
	seq.604	350 (Rep78/68)	AAT
		350	AAT
	500 <b>60</b> 5	350	AAT
40	seq.605	350 (Rep78/68)	GCT.
40		350 350	GCT
	seq.606		GCT
	004.000	354 <sup>.</sup> (Rep78/68) 354	GCC GCC
		354	
45	seq.607	363 (Rep78/68)	GCC
		363	GCC
		363	GCC GCC
	seq.608	364 (Rep78/68)	GCT
		364	GCT
50		364	GCT
	seq.609	367 (Rep78/68)	GCC

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		367	GCC
	610	367	GCC
	seq.610	370 (Rep78/68)	GCC
5	•	370	GCC
	seq.61 <b>1</b>	370 376 (Rep78/68)	GCC
	3eq.011	376 (Rep78/08) 376	GCG
		376	GCG GCG
	seq.612	381 (Rep78/68)	GCG
10		381	GCG
		381	GCG
	seq.613	382 (Rep78/68)	GCG
	• • • •	382	GCG
		382	GCG
15	seq.614	389 (Rep78/68)	GCG
		389	GCG
		389	GCG
	seq.615	407 (Rep78/68)	GCC
		407	GCC
20	•	407	GCC
	seq.616	411 (Rep78/68)	GCA
		411	GCA
		411	· GCA
25	seq.617	414 (Rep78/68)	GCT
25		414	GCT
	000 610	414	GCT
	seq.618	420 (Rep78/68)	GCT
		420 420	GCT
30	seq.619	421 (Rep78/68)	GCT GCC
	004.010	421 (Nep76/06)	GCC
	-	421	GCC
	seq.620	422 (Rep78/68)	GCC
	•	422	GCC
35		422	GCC
	seq.621	424 (Rep78/68)	GCG
		424	GCG
		424	GCG
	seq.622	428 (Rep78/68)	GCT
40		428	GCT
		428	GCT
	seq.623	429 (Rep78/68)	GCC
		429	GCC
45	604	429	GCC
43	seq.624	438 (Rep78/68)	GCG
		438	GCG
	sea 625	438	GCG
	seq.625	440 (Rep78/68) 440	GCG
50		440	GCG
~ ~	seq.626	451 (Rep78/68)	GCG GCC
			GCC

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		451	GCC
	seg.627	451	GCC
	304.027	460 (Rep78/68) 460	GCG
	5	460	GCG
	seq.628	462 (Rep78/68)	GCC
		462	GCC
		462	GCC
10	seq.629	462 (Rep78/68)	ATA
- 10	,	462	ATA
	seq.630	462 484 (Rep78/68)	ATA
	304.000	484 (Rep76/68)	GCC
		484	GCC
15	seq.631	488 (Rep78/68)	GCG
	·	488	GCG
		488	GCG
	seq.632	495 (Rep78/68)	GCC
		495	GCC
20		495	GCC
	seq.633	497 (Rep78/68)	GCC
		497	GCC
	seq.634	497 497 (Rep78/68)	GCC
25	504,004	497 (Nep76/66)	CGA CGA
		497	CGA
	seq.635	497 (Rep78/68)	CTC
		497	СТС
		497	CTC
30	seq.636	497 (Rep78/68)	TAC
	_	497	TAC
	 500 637	497	TAC
	seq.637	498 (Rep78/68) 498	GCT
35		498	GCT GCT
	seq.638	499 (Rep78/68)	GCC
		499	GCC
		499	GCC
40	seq.639	503 (Rep78/68)	GCG
40		503	GCG
	C10	503	GCG
	seq.640	510 (Rep78/68)	GCA
		510 510	GCA
45	seq.641	510 511 (Rep78/68)	GCA GCA
		511	GCA
		511	GCA
	seq.642	512 (Rep78/68)	GCT
		512	GCT
50	240	512	GCT
	seq.643	516 (Rep78/68)	GCG

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		516	GCG
		516	GCG
	seq.644	517 (Rep78/68)	. GCT
-		517	GCT
5		517	GCT
	seq.645	517 (Rep78/68)	AÁC
		517	AAC
	000 646	517	AAC
10	seq.646	518 (Rep78/68)	GCA
		518 618	GCA
	seq.647	518 519 (Rep78/68)	GCA
	364.047	519 (Rep76/66) 519	GCG
	-	519	GCG
15	seq.648	598 (Rep78/68)	GCG GCA
	seq.649	600 (Rep78/68)	GCG -
	seq.650	601 (Rep78/68)	GCA
	seq.651	335 420 495	GCT GCC GCC
		335 420 495	GCT GCC GCC
20		335 420 495	GCT GCC GCC
	seq.652	39 140	GCA GCC
	seq.653	279 428 451	GCC GCT GCC
		279 428 451	GCC GCT GCC
		279 428 451	GCC GCT GCC
25	seq.654	125 237 600	GCG GCC GCG
	•	125 237 600	GCG GCC GCG
		125 237 600	GCG GCC GCG
	seq.655	163 259	GCT GCG
20		163 259	GCT GCG
30		163 259	GCT GCG
	seq.656	17 127 189	GCG GCT GCG
	seq.657	350 428	GCT GCT
		350 428	GCT GCT
35	00m 6E9	350 428	GCT GCT
33	seq.658	54 338 495	GCC GCC GCC
		54 338 495 54 338 405	GCC GCC GCC
	seq.659	54 338 495 350 420	GCC GCC GCC
	004.005	350 420	GCT GCC
40		350 420	GCT GCC
	seq.660	189 197 518	GCG GCG GCA
		189 197 518	GCG GCG GCA
		189 197 518	GCG GCG GCA
	seq.661	468 516	GCC GCG
45		468 516	GCC GCG
		468 516	GCC GCG
	seq.662	127 221 350 54 140	GCT GCA GCT GCC GCC
		127 221 350 54 140	GCT GCA GCT GCC GCC
		127 221 350 54 140	GCT GCA GCT GCC GCC
50	seq.663	221 285	GCA GCG
		221 285	GCA GCG

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		801.00	
	seq.664	221 285	GCA GCG
	3eq.004	23 495	GCT GCC
		23 495	GCT GCC
5	seq.665	23 495 20 54 420 495	GCT GCC
. `	304.005	20 54 420 495	GCC GCC GCC
		20 54 420 495	GCC GCC GCC GCC
	seq.666	412 612	GCC GCC GCC GCC
	004.000	412 612	GCC GCG GCC GCG
10	,	412 612	GCC GCG
	seq.667	197 412	GCG GCC
		197 412	GCG GCC
		197 412	GCG GCC
	seq.668	412 495 511	GCC GCC GCA
15		412 495 511	GCC GCC GCA
		412 495 511	GCC GCC GCA
	seq.669	98 422	GCC GCC
	.,	98 422	GCC GCC
		98 422	GCC GCC
20	seq.670	17 127 189	GCG GCT GCG
	seq.671	20 54 495	GCC GCC GCC
	•	20 54 495	GCC GCC GCC
	•	20 54 495	GCC GCC GCC
	seq.672	54 163	GCC GCT
25	seq.673	259 54	GCG GCC
		259 54	GCG GCC
		259 54	GCG GCC
	seq.674	335 399	GCT GCG
	•	335 399	GCT GCG
30	seq.675	335 399	GCT GCG
		221 432	GCA GCA
		221 432	GCA GCA
	ı	221 432	GCA GCA
	seq.676 '	259 516	GCG GCG
35		259 516	GCG GCG
		259 516	GCG GCG
	seq.677	495 516	GCC GCG
		495 516	GCC GCG
40		495 516	GCC GCG
40	seq.678	414 14	GCT GCC
		414 14	GCT GCC
	670	414 14	GCT GCC
	seq.679	74 402 495	GCG GCC GCC
45		74 402 495	GCG GCC GCC
73	ssa 690	74 402 495	GCG GCC GCC
	seq.680	228 462 497	GCC GCC GCC.
		228 462 497	GCC GCC GCC
	seq.681	228 462 497 290 338	GCC GCC GCC
50	004.001	290 338	GCG GCC
		290 338 290 338	GCG GCC
		230 330	GCG GCC

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		,	
	seq.682	140 511 140 511	GCC GCA GCC GCA
		140 511	
	seq.683		GCC GCA
1	5 seq.003	86 378	GCG GCG
,	5	86 378	GCG GCG
		86 378	GCG GCG
	seq.684	54 86	GCC GCG
		54 86	GCC GCG
	_	54 86	GCC GCG
10	) seq.685	214 495 140	GCG GCC GCC
		214 495 140	GCG GCC GCC
		214 495 140	GCG GCC GCC
	seq.686	495 511	GCC GCA
	•	495 511	GCC GCA
15	5	495 511	
	seq.687	495 54	GCC GCA
*	554.557		GCC GCC
		495 54	GCC GCC
	500 600	495 54	GCC GCC
20	seq.688	197 495	GCG GCC
20		197 495	GCG GCC
		197 495	GCG GCC
	seq.689	261 20	GCC GCC
		261 20	GCC GCC
		261 20	GCC GCC
25	seq.690	54 20	GCC GCC
	seq.691	197 420	GCG GCC
		197 420	GCG GCC
		197 420	GCG GCC
	seq.692	54 338 495	GCC GCC GCC
30		54 338 495	GCC GCC GCC
		54 338 495	GCC GCC GCC
	seq.693	197 427	GCG GCG
		197 427	
		197 427	GCG GCG
35	seq.694		GCG GCG
	004.004	54 228 370 387	GCC GCC GCC GCG
		54 228 370 387	GCC GCC GCC GCG
	500 605	54 228 370 387	GCC GCC GCC GCG
	seq.695	221 289	GCA GCC
40		221 289	GCA GCC
40	000	221 289	GCA GCC
	seq.696	54 163	GCC GCT
		54 163	GCC GCT
	seq.697	341 407 420	GCC GCC GCC
4-		341 407 420	GCC GCC GCC
45		341 407 420	GCC GCC GCC
	seq.698	54 228	GCC GCC
		54 228	GCC GCC
		54 228	GCC GCC
	seq.699	96 125 511	GCA GCG GCA
50		96 125 511	GCA GCG GCA
		96 125 511	GCA GCG GCA
			AND BUD AND

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	seq.700	197 420	GCG GCC
		197 420	GCG GCC
	704	197 420	GCG GCC
	seq.701	334 428 499	GCG GCT GCC
•	•	334 428 499	GCG GCT GCC
	700	334 428 499	GCG GCT GCC
	seq.702	197 414	GCG GCT
		197 414	GCG GCT
10	) 702	197 414	GCG GCT
10		30 54 127	GCG GCC GCT
	seq.704	29 260	GCG GCG
	•	29 260	GCG GCG
	200 700	29 260	GCG GCG
15	seq.706	4 484	GCT GCC
	,	4 484	GCT GCC
	. 707	4 484	GCT GCC
	seq.707	258 124 132	GCC GCC GCC
		258 124 132	GCC GCC GCC
20		258 124 132	GCC GCC GCC
20	seq.708	231 497	GCC GCC
		231 497	GCC GCC
		231 497	GCC GCC
	seq.709	221 258	GCA GCC
25		221 258	GCA GCC
25	744	221 258	GCA GCC
	seq.710	234 264 326	GCG GCG GCC
		234 264 326	GCG GCG GCC
		234 264 326	GCG GCG GCC
20	seq.711	153 398	AGC GCG
30	·	153 398	AGC GCG
		153 398	AGC GCG
	seq.712	<b>5</b> 3 216	GCG GCC
	seq.713	22 382	GCT GCG
35		22 382	GCT GCG
39	744	22 382	GCT GCG
	seq.714	231 411	GCC GCA
		231 411	GCC GCA
	22- 715	231 411	GCC GCA
40	seq.715	59 305	GCG GCC
40		59 305	GCG GCC
	710	59 305	GCG GCC
	seq.716	53 231	GCG GCC
		53 231	GCG GCC
45	227	53 231	GCG GCC
45	seq.717	258 498	GCC GCT
		258 498	GCC GCT
	seq.718	258 498	GCC GCT
	364.710	88 231	GCC GCC
50		88 231	GCC GCC
	seg 710	88 231	GCC GCC
	seq.719	101 363	GCA GCC

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		101 363	GCA GCC
		101 363	GCA GCC
	seq.720	354 132	GCC GCC
		354 132	GCC GCC
5		354 132	GCC GCC
	seq.726	598	GAC
	seq.727	598	AGC
	seq.728	600	CCG

The above nucleic acid molecules are provided in plasmids, which 10 are introduced into cells to produce the encoded proteins. The analysis revealed the amino acid positions that affect Rep proteins activities. Changes of amino acids at any of the hit positions result in altered protein activity. Hit positions are numbered and referenced starting from amino acid 1 (nucleotide 321 in AAV-2 genome), also codon 1 of the protein 15 Rep78 coding sequence under control of p5 promoter of AAV-2: 4, 20, 22, 29, 32, 38, 39, 54, 59, 124, 125, 127, 132, 140, 161, 163, 193, 196, 197, 221, 228, 231, 234, 258, 260, 263, 264, 334, 335, 337, 342, 347, 350, 354, 363, 364, 367, 370, 376, 381, 389, 407, 411, 414, 420, 421, 422, 424, 428, 438, 440, 451, 460, 462, 484, 488, 495, 497, 498, 499, 503, 511, 512, 516, 517, 518, 542, 548, 598, 20 600 and 601. The encoded Rep78, Rep68, Rep 52 and Rep 40 proteins and rAAV encoding the mutant proteins are provided. The corresponding nucleic acid molecules, Rep proteins, rAAV and cells containing the nucleic acid molecules or rAAV in which the native proteins are from other AAV serotypes, including, but are not limited to, AAV-1, AAV-3, 25 AAV-3B, AAV-4, AAV-5 and AAV-6.

Other hit positions identified include: 10, 64, 74, 86, 88, 101, 175, 237, 250, 334, 429 and 519.

Also provided are nucleic acid molecules, the rAAV that encode
the mutant proteins, and the encoded proteins in which the native amino
acid at each hit position is replaced with another amino acid, or is
deleted, or contains additional amino acids at or adjacent to or near the

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hit positions. In particular the following nucleic acid molecules and rAAV that encode proteins containing the following amino acid replacements or combinations thereof: T by N at Hit position 350; T by I at Hit position 462; P by R at Hit position 497; P by L at Hit position 497; P by Y at Hit position 497; T by N at Hit position 517; L by S at hit position 542; R by S at hit position 548; G by D at Hit position 598; G by S at Hit position 598; V by P at Hit position 600; in order to increase Rep proteins activities in terms on AAV or rAAV productivity. The corresponding nucleic acid molecules, recombinant Rep proteins from the other serotypes and the resulting rAAV are also provided (see Figs. 3 and the above Table for the corresponding position in AAV-1, AAV-3, AAV-3B, AAV-4, AAV-5 and AAV-6).

Mutant adeno-associated virus (AAV) Rep proteins and viruses encoding such proteins that include mutations at one or more of residues 64, 74, 88, 175, 237, 250 and 429, where residue 1 corresponds to residue 1 of the Rep78 protein encoded by nucleotides 321-323 of the AAV-2 genome, and where the amino acids are replaced as follows: L by A at position 64; P by A at position 74; Y by A at position 88; Y by A at position 175; T by A at position 237; T by A at position 250; D by A at position 429 are provided. Nucleic acid molecules encoding these viruses and the mutant proteins are also provided.

Also provided are nucleic acid molecules produced from any of the above-noted nucleic acid molecules by any directed evolution method, including, but are not limited to, re-synthesis, mutagenesis, recombination and gene shuffling and any way by combining any combination of the molecules, *i.e.*, one, two by one, two by two, ......n by n, where n is the number of molecules to be combined ( *i.e.*, combining all together). The resulting recombinant AAV and encoded proteins are also provided.

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Also provided are nucleic acid molecule in which additional amino acids surrounding each hit, such as one, two, three . . . ten or more, amino acids are systematically replaced, such that the resulting Rep protein(s) has increased or decreased activity. Increased activity as assessed by increased recombinant virus production in suitable cells is of particular interest for production of recombinant viruses for use, for example, in gene therapy.

Also provided are combinations of the above noted mutants in which several of the noted amino acids are changed and optionally additional amino acids surrounding each hit, such as one, two, three . . . ten or more, are replaced.

For all of the mutant proteins provided herein those with increased activity, such as an increase in titer of rAAV when virus containing such mutations and/or expressing such mutant proteins are replicated, are of particular interest. Such mutations and proteins are provided herein and may be made by the methods herein, including by combining any of the mutations provided herein to produce additional mutant proteins that have altered biological activity, particularly increased activity, compared to the wild-type.

15

The nucleic acid molecules of SEQ ID Nos. 563-725 and the encoded proteins (SEQ ID Nos. 1-562 and 726-728) are also provided. Recombinant AAV and cells containing the encoding nucleic acids are provided, as are the AAV produced upon replication of the AAV in the cells.

Methods of *in vivo* or *in vitro* production of AAV or rAAV using any of the above nucleic acid molecules or cells for intracellular expression of rep proteins or the rep gene mutants are provided. *In vitro* production is effected using cell free systems, expression or replication

and/or virus assembly. *In vivo* production is effected in mammalian cells that also contain any requisite *cis* acting elements required for packaging.

Also provided are nucleic acid molecules and rAAV (any serotype) in which position 630 (or the corresponding position in another serotype; see Figs. 3 and the table above) has been changed. Changes at this position and the region around it lead to changes in the activity or in the quantities of the Rep or Cap proteins and/or the amount of AAV or rAAV produced in cells transduced with AAV encoding such mutants. Such mutations include tgc to gcg change (SEQ ID No. 721). Mutations at any position surrounding the codon position 630 that increase or decrease the Rep or Cap proteins quantities or activities are also provided. Methods using the rAAV (any serotype) that contain nucleic acid molecules with a mutation at position 630 or within 1, 2, 3 . . . . 10 or more bases thereof for the intracellular expression rep proteins or the rep gene mutants

15 covered by claims 10 to 13, for the production of AAV or rAAV (either in vitro, in vivo or ex vivo) are provided. In vitro methods include cell free systems, expression or replication and/or virus assembly.

Also provided are rAAV (and other serotypes with corresponding changes) and nucleic acid molecules encoding an amino acid replacement by N at Hit position 350 of AAV-1, AAV-3, AAV-3B, AAV-4 and AAV-6 or at Hit position 346 of AAV-5; by I at Hit position 462 of AAV-1, AAV-3, AAV-3B, AAV-4 and AAV-6 or at Hit position 458 of AAV-5; by either R, L or Y at Hit position 497 of AAV-1, AAV-3, AAV-3B, AAV-4 and AAV-6 or at Hit position 493 of AAV-5; by N at Hit position 517 of AAV-1, AAV-3, AAV-3B, AAV-4 and AAV-6 or at Hit position 535 of AAV-5; by S at hit position 543 of AAV-1 and AAV-6 or at hit position 542 of AAV-3, AAV-3B and AAV-4 or at hit position 548 of AAV-3, AAV-3B and AAV-4 or at hit position 548 of AAV-3, AAV-3B and AAV-4 or at hit position 548 of AAV-3, AAV-3B and AAV-4 or at hit position 548 of AAV-3, AAV-3B and AAV-4 or at hit position 549 of AAV-1 or at hit position 549 of AAV-1.

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Hit position 599 of AAV-1, AAV-4 and AAV-6 or at Hit position 600 of AAV-3 and AAV-3B; by P at Hit position 602 of AAV-1, AAV-4 and AAV-6 or at hit position 603 of AAV-3 and AAV-3B or at hit position 589 of AAV-5 in order to increase Rep proteins activities as assessed by AAV or rAAV productivity. Methods using such AAV for expression of the encoded proteins and production of AAV are also provided.

Since modifications will be apparent to those of skill in this art, it is intended that this invention be limited only by the scope of the appended claims.

## WHAT IS CLAIMED IS:

- 1. An adeno-associated virus (AAV), comprising nucleic acid encoding the sequence of amino acids in any of SEQ ID Nos. 1-562 and 726-728 or encoding a sequence of amino acids encoded by SEQ ID Nos. 722-725.
- 2. The AAV of claim 1, wherein the sequence of nucleotides encoding the sequence of amino acids is set forth in SEQ ID Nos. 563-725.
- The AAV of claim 1 that has an altered activity in a Rep
   protein and/or a capsid protein.
  - 4. The AAV of claim 3, wherein the alteration leads to greater activity in the Rep gene manifested as an increased titer of virus upon introduction and replication in a host cell compared to the titer of virus upon introduction and replication of a wild type Rep gene.
- 5. The AAV of claim 1 that is of serotype AAV-1, AAV-2, AAV-3, AAV-3B, AAV-4, AAV-5 or AAV-6.
  - A mutant adeno-associate virus (AAV) Rep protein,
     comprising mutations at one or more of residues 4, 20, 22, 29, 32, 38, 39, 54, 59, 124, 125, 127, 132, 140, 161, 163, 193, 196, 197, 221,
- 20 228, 231, 234, 258, 260, 263, 264, 334, 335, 337, 342, 347, 350, 354, 363, 364, 367, 370, 376, 381, 389, 407, 411, 414, 420, 421, 422, 424, 428, 438, 440, 451, 460, 462, 484, 488, 495, 497, 498, 499, 503, 511, 512, 516, 517, 518, 542, 548, 598, 600 and 601 of AAV-2 or the corresponding residues in other serotypes, wherein residue
  25 1 corresponds to residue 1 of the Rep78 protein encoded by nucleotides
- 1 corresponds to residue 1 of the Rep78 protein encoded by nucleotides 321-323 of the AAV-2 genome, wherein the mutations comprise insertions, deletions or replacements of the native amino acid residue(s).
  - 7. The Rep protein of claim 6 that is Rep 78, Rep 68, Rep 52 or Rep 40.

- 8. The mutant AAV Rep protein of claim 6, wherein the AAV is an AAV-1, AAV-2, AAV-3, AAV-3b, AAV-4, AAV-5 or AAV-6, wherein the mutation is in the equivalent position in each serotype, wherein the listed residues are the positions in AAV-2.
- 9. A mutant AAV Rep protein of claim 6 that has increased activity compared to the native protein, wherein activity is assessed by measuring viral production when an AAV that encodes the protein is introduced into a cell under conditions wherein the virus replicates.
- 10. A mutant AAV Rep protein of claim 6 that has decreased activity compared to the native protein, wherein activity is assessed by measuring viral production when an AAV that encodes the protein is introduced into a cell under conditions wherein the virus replicates.
  - 11. A mutant Rep protein of claim 6, further comprising a mutation at one or more of residues 10, 64, 74, 86, 88, 101, 175, 237, 250, 334, 429 and 519.
- 12. The mutant Rep protein of claim 6, wherein the amino acids are replaced as follows: T by N at position 350; T by I at position 462; P by R at position 497; P by L at position 497; P by Y at position 497; T by N at position 517; G by D at position 598; G by S at position 598; V by P at position 600, whereby the activity of the Rep protein is increased as assessed by rAAV production compared to the native Rep protein.
  - 13. A mutant Rep protein of claim 6, comprising two or more of the mutations.
- 14. A mutant adeno-associate virus (AAV) Rep protein,
  25 comprising mutations at one or more of residues 64, 74, 88, 175, 237,
  250 and 429, wherein: residue 1 corresponds to residue 1 of the Rep78 protein encoding by nucleotides 321-323 of the AAV-2 genome;

wherein the amino acids are replaced as follows:

L by A at position 64;

P by A at position 74; Y by A at position 88; Y by A at position 175; T by A at position 237;

T by A at position 250;

D by A at position 429;

the mutations comprise insertions, deletions or replacements of the native amino acid residue.

- 15. A nucleic acid molecule encoding the protein of claim 6.
- 10 16. A recombinant AAV comprising the nucleic acid molecule of claim 15.
  - 17. A eukaryotic cell, comprising the recombinant AAV of claim 16.
- 18. A collection of nucleic acid molecules comprising a plurality of the molecules of claim 17.
  - 19. A collection of nucleic acid molecules comprising a plurality of the molecules of claim 15.
- 20. An isolated nucleic acid molecule encoding the proteins of SEQ ID Nos. 1-562 and 726-728 or encoding a sequence of amino acids encoded by SEQ ID Nos. 722-725.
  - 21. A Rep protein of any of SEQ ID Nos. 1-562 and 726-728 or encoding a sequence of amino acids encoded by SEQ ID Nos. 722-725.
    - 22. A Rep protein encoded by any of SEQ ID Nos. 564-725.
- 23. A method for intracellular expression of a mutant Rep protein, comprising:

introducing the recombinant AAV of claim 16 into a host cell; and

culturing the cell, under conditions and in which the AAV Rep proteins are expressed.

- 24. The method of claim 23, wherein the AAV replicates.
- 25. An AAV genome, comprising a mutation at one or more of nucleotides corresponding to nucleotides 2209-2211 of the AAV-2 genome, which encode amino acid residue 630 of the Rep78 protein, wherein:

the mutation is a deletion, insertion or replacement of a nucleotide; and the mutation results in a change in the activity or in the quantities of the Rep or Cap proteins as assessed by the level of replication of the AAV genome.

- 10 26. The AAV genome of claim 25, wherein the mutation at position 630 is a tgc to gcg and the intron comprises the sequence (SEQ ID No. 722):
- 27. The AAV genome of claim 25, wherein the mutation at20 position 630 is a tgc to cgc and the intron comprises the sequence (SEQ ID No. 723):

- 28. The AAV genome of claim 25, wherein the mutation at position 630 is a tgc to cct and the intron comprises the sequence (SEQ ID No. 724):
- gtaccaaaacaaatgttctcgtcacgtgggcatgaatctgatgctgttt

  ccctgcagacaatgcgagagaatgaatcagaattcaaatatctgcttcac
  tcacggacagaaagactgtttagagtgctttcccgtgtcagaatctcaac
  ccgtttctgtcgtcaaaaaggcgtatcagaaactgtgctacattcatcat
  atcatgggaaaggtgccagacgcttgcactgcctgcgatctggtcaatgt
  ggatttggatgactgcatctttgaacaataaatgatttaaatcaggt
  atggccctcgatggttatcttccag.
  - 29. The AAV genome of claim 25, wherein the mutation at position 630 is a tgc to tca and the intron comprises the sequence (SEQ ID No. 725):
- gtaccaaaacaaatgttctcgtcacgtgggcatgaatctgatgctgtttcc

  15 ctgcagacaatgcgagagaatgaatcagaattcaaatatctgcttcactca
  cggacagaaagactgtttagagtgctttcccgtgtcagaatctcaacccgt
  ttctgtcgtcaaaaaggcgtatcagaaactgtgctacattcatcatatcat
  gggaaaggtgccagacgcttgcactgcctgcgatctggtcaatgtggattt
  ggatgactgcatctttgaacaataaatgatttaaatcaggtatggctcacg

  20 atggttatcttccag.
  - 30. A method for intracellular expression of a mutant Rep protein, comprising:
  - introducing the recombinant AAV of claim 25 into a host cell; and
- culturing the cell, under conditions and in which the AAV Rep proteins and/or cap proteins are expressed.
  - 31. The method of claim 30, wherein the AAV replicates.
  - 32. The AAV genome of claim 25, wherein the AAV is of serotype AAV-1, AAV-3, AAV-3B, AAV-4, AAV-5 or AAV-6.

- 33. A method of titering virus by a method designated tagged replication and expression enhancement, comprising:
- (i) incubating host cells with a reporter virus vector and with a titering virus of unknown titer, wherein a titering virus increases or decreases the output signal from the reporter virus; and
- (ii) measuring the output signal of the reporter virus and determining the titer of the reporter virus; and
- (ii) determining the titer of the titering virus bycomparing the titer of the reporter virus in the presence and absence ofthe titering virus.
  - 34. A process for the production of an adeno-associated virus (AAV) protein or a recombinant AAV having a predetermined property, comprising:
- (a) producing a population of sets of nucleic acid molecules thatencode modified forms of a target protein;
  - (b) introducing each set of nucleic acid molecules into host cells and expressing the encoded protein, wherein the host cells are present in an addressable array;
- (c) individually screening the sets of encoded proteins to identify
   one or more proteins that have activity that differs from the target protein, wherein each such protein is designated a hit;
  - (d) modifying the nucleic acid molecules that encode the hits, to produce a set of nucleic acid molecules that encode modified hits, wherein the nucleic acid molecules comprise rAAV vectors;
- (e) introducing the each set of nucleic acids that encode the modified hits into cells; and
  - (f) individually screening the sets of cells that contain the nucleic acid molecules that encode the modified hits to identify one or more cells that encodes a protein that has activity that differs from the target protein

and has properties that differ from the original hits, wherein each such protein is designated a lead.

- 35. The process of claim 34, wherein the cells are eukaryotic cells that are transduced with the vectors.
- 5 36. The method of claim 35, wherein at step (f) the titer of the viral vectors in each set of cells is determined.
  - 37. The method of claim 36, wherein the target protein is a protein involved in viral replication.
- 38. The method of claim 37, wherein the target protein is a Rep. 10 protein.
  - 39. The AAV mutant Rep protein of claim 6 that binds to a sequence from a papillomavirus, oncogene or human immunodeficiency virus (HIV) with different affinity from a wild-type AAV Rep protein.
- 40. A fusion protein, comprising the *tat* protein of HIV and the mutant Rep protein of claim 39.
  - 41. The fusion protein of claim 40, wherein the HIV is HIV-1.
  - 42. A pharmaceutical composition, comprising the protein of claim 39 in a pharmaceutically acceptable carrier.
- 43. A recombinant adeno-associated virus (rAAV) that encodes
  20 a mutant Rep protein that has increased activity, wherein increased
  activity of a Rep protein is manifested as an increased titer of virus upon
  introduction and replication in a host cell compared to the titer of virus
  upon introduction and replication of a wild type Rep gene.
- 44. A mutant AAV Rep protein that has increased activity,
  wherein increased activity of a Rep protein is manifested as an increased titer of virus upon introduction and replication in a host cell compared to the titer of virus upon introduction and replication of a wild type Rep gene.

- 45. A nucleic acid molecule that encodes that mutant Rep protein of claim 44.
  - 46. A cell, comprising the nucleic acid molecule of claim 45.
  - 47. A rAAV, comprising the nucleic acid molecule of claim 45.
- 5 48. A cell, comprising the rAAV of claim 47.
  - 49. A method for production of rAAV, comprising:

introducing the rAAV of claim 47 into a cell under conditions whereby the virus replicates to produce encapsulated rAAV.

- 50. A method for the production of mutant Rep protein comprisingexpressing the nucleic acid molecule of claim 45.
  - 51. The method of claim 50, wherein expression is effected in vivo.
  - 52. The method of claim 50, wherein expression is effected in vitro.
- 15 53. A method for producing Rep protein in a host cell, comprising: expressing the protein encoded by the nucleic acid encoding the protein of claim 44, wherein the method is performed in vitro or in vivo.
- 54. The method of claim 53, wherein the nucleic acid is 20 introduced into a cell.
  - 55. The method of claim 53, wherein expression is effected in a cell-free system.
- 56. A method of treating or inhibiting infection by human papilloma virus or a human immunodeficiency virus, comprising
  25 administering, to a subject exposed to the virus or infected with the virus, a composition containing a rAAV of claim 47.
  - 57. A nucleic acid molecule encoding the protein of claim 7.
  - 58. A nucleic acid molecule encoding the protein of claim 8.
  - 59. A nucleic acid molecule encoding the protein of claim 9.

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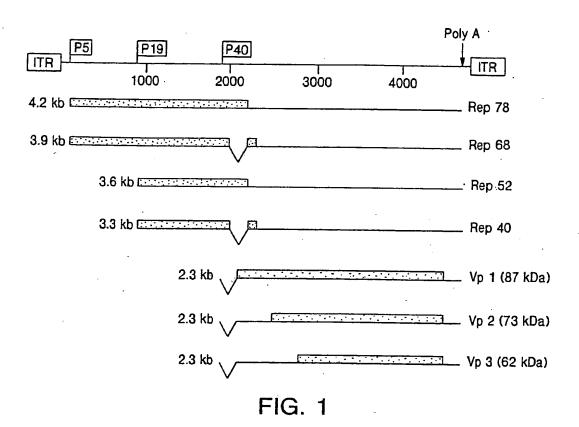
	60.	A nucleic acid molecule encoding the protein of claim 10.
	61.	A nucleic acid molecule encoding the protein of claim 11.
	62.	A nucleic acid molecule encoding the protein of claim 12.
	63.	A nucleic acid molecule encoding the protein of claim 13.
5	64.	
	65.	A recombinant AAV comprising the nucleic acid molecule of
	claim 57.	
	66.	A recombinant AAV comprising the nucleic acid molecule of
	claim 58.	
10	67.	A recombinant AAV comprising the nucleic acid molecule of
	claim 59.	
	68.	A recombinant AAV comprising the nucleic acid molecule of
	claim 60.	
	69.	A recombinant AAV comprising the nucleic acid molecule of
15	claim 61.	
	70.	A recombinant AAV comprising the nucleic acid molecule of
	claim 62.	
	71.	A recombinant AAV comprising the nucleic acid molecule of
	claim 63.	
20	72.	A recombinant AAV comprising the nucleic acid molecule of
	claim 64.	
	73.	A cell, comprising the recombinant AAV of claim 65.
	74.	A cell, comprising the recombinant AAV of claim 66.
	75.	A cell, comprising the recombinant AAV of claim 67.
25	76.	A cell, comprising the recombinant AAV of claim 68.
	77.	A cell, comprising the recombinant AAV of claim 69.
	78.	A cell, comprising the recombinant AAV of claim 70.
	79.	A cell, comprising the recombinant AAV of claim 71.
	80.	A cell, comprising the recombinant AAV of claim 72.

81. A method for intracellular expression of a mutant Rep protein, comprising:

culturing the cell of claim 73 under conditions and in which the AAV Rep proteins are expressed.

- 5 82. The method of claim 81, wherein the AAV replicate.
  - 83. A method for intracellular expression of a mutant Rep protein, comprising culturing the cell of claim 74 under conditions in which the AAV Rep proteins are expressed.
    - 84. The method of claim 83, wherein the AAV replicate.
- 10 85. A method of altering expression of a gene, comprising contacting the gene with a mutant rep protein that has increased activity, wherein increased activity of a Rep protein is manifested as an increased titer of virus upon introduction and replication in a host cell compared to the titer of virus upon introduction and replication of a wild type Rep gene.
  - 86. The method of claim 85, wherein the gene is a viral gene.
  - 87. The method of claim 85, wherein the gene is a cellular gene.
  - 88. The mutant protein of claim 6, wherein serotype is AAV-1, AAV-2, AAV-3, AAV-3B, AAV-4, AAV-5 or AAV-6.
- 20 89. The protein of claim 44, wherein the mutation is at a residue corresponding to one or more of residues 350, 462, 497, 517, 542, 548, 598, 600 and 630 of AAV-2.
  - 90. The mutant protein of claim 89, wherein serotype is AAV-1, AAV-2, AAV-3, AAV-3B, AAV-4, AAV-5 or AAV-6.
- 91. The AAV mutant Rep protein of claim 44 that binds to a sequence from a papillomavirus, oncogene or human immunodeficiency virus (HIV) with different affinity from a wild-type AAV Rep protein.
  - 92. A pharmaceutical composition, comprising the protein of claim 91 in a pharmaceutically acceptable carrier.

93. A pharmaceutical composition, comprising the rAAV of claim 47 in a pharmaceutically acceptable carrier.



Hits on Rep

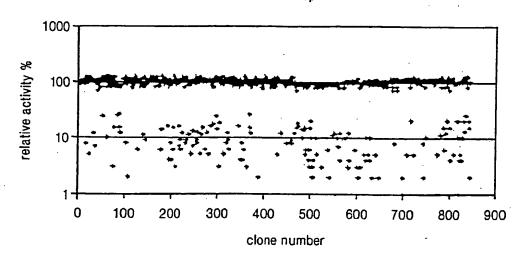


FIG. 2A

## Lead positions on Rep

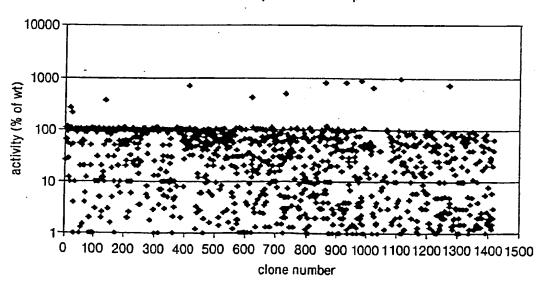


FIG. 2B

	10 20 30 40 50 60	
1	MPGFYEIVIKVPSDLDEHLPGISDSFVSWVAEKEWELPPDSDMDLNLIEQAPLTVAEKLQ-	- 60
2	MPGFYEIVIKVPSDLDEHLPGISDSFVNWVAEKEWELPPDSDMDLNLIEOAPLTVAEKLO	60
3	MPGFYEIVLXVPSDLDEHLPGISNSFVNWVAEKEWELPPDSDMDPNLIEQAPLTVAEKLQ	60
4	MPGFYEIVLKVPSDLDEHLPGISNSFVNWVAEKEWELPPDSDMDPNLIEQAPLTVAEKLQ	60
5	MPGFYEIVLKVPSDLDEHLPGISDSFVSWVAFKEWELPPDSDMDLNLIEOAPLTVAEKLO	60
6	MPGFYEIVIKVPSDLDGHLPGISDSFVNWVAEKEWELPPDSDMDLNLIEOAPLTVAEKLO	60
7	MATFYEVIVRVPFDVEEHLPGISDSFVDWVTGQIWELPPESDLNLTLVEQPQLTVADRIR	60
ć	M**FYE**:*VP*D***HLPGIS+SFV:WV****WELPP*SD**+*L*EQ**LTVA****	80
_	70 80 90 100 110 120	
1	RDFLVQWRRVSKAPEALFFVQFEKGESYFHLHILVETTGVKSMVLGRFLSQIRDKLVQTI	120
2	RDFLVQWRRVSKAPEALFFVQFEKGESYFHLHILVETTGVKSMVLGRFLSQIRDKLVQTI	120
3	REFLVEWRRVSKAPEALFFVQFEKGETYFHLHVLIETIGVKSMVVGRYVSQIKEKLVTRI	120
4	REFLVEWRRVSKAPEALFFVQFEKGETYFHLHVLIETIGVKSMVVGRYVSQIKEKLVTRI	120
5	REFLVEWRRVSKAPEALFFVQFEKGDSYFHLHILVETVGVKSMVVGRYVSQIKEKLVTRI	120
6	RDFLTEWRRVSKAPEALFFVQFEKGESYFHMHVLVETTGVKSMVLGRFLSQIREKLIQRI	120
7	RVFLYEWNKFSKQ-ESKFFVQFEKGSEYFHLHTLVETSGISSMVLGRYVSQIRAQLVKVV	119
Ċ	R:FL++W***SK**E**FFVQFEKG+:YFH*H:L+ET:G**SMV:GR::SOI::*L*::*	
_	MILLIAN ON B III VEIDMONIII MILLIANIO OMA GRANGELLI II II	
	130 140 150 160 170 180	
1	YRGIEPTLPNWFAVTKTRNGAGGGNKVVDECYIPNYLLPKTQPELQWAWTNMEEYISACL	180
2	YRGIEPTLPNWFAVTKTRNGAGGGNKVVDECYIPNYLLPKTOPELOWAWTNMEEYISACL	180
3	YRGVEPQLPNWFAVTKTRNGAGGGNKVVDDCYIPNYLLPKTQPELQWAWTNMDQYLSACL	180
4	YRGVEPQLPNWFAVTKTRNGAGGGNKVVDDCYIPNYLLPKTQPELQWAWTNMDQYLSACL	180
5	YRGVEPQLPNWFAVTKTRNGAGGGNKVVDDCYIPNYLLPKTQPELQWAWTNMDQYISACL	180
6	YRGIEPTLPNWFAVTKTRNGAGGGNKVVDECYIPNYLLPKTQPELQWAWTNMEQYLSACL	180
7	FQGIFPQINDWVAITKVKKGGANKVVDSGYIPAYLLPKVOPELOWAWTNLDEYKLAAL	177
Ċ	**G:EP:***W*A*TK*****GG*NKVVD:*YIP*YLLPK*QPELQWAWTN*::Y:*A*L	
_		
	190 200 210 220 230 240	
1	NLAERKRLVAQHLTHVSQTQEQNKENLNPNSDAPVIRSKTSARYMELVGWLVDRGITSEK	240
2	NLAERKRLVAHDLTHVSQTQEQNKENLNPNSDAPVIRSKTSARYMELVGWLVDRGITSEK	240
3	NLAERKRLVAQHLTHVSQTQEQNKENQNPNSDAPVIRSKTSARYMELVGWLVDRGITSEK	240
4	NLAERKRLVAQHLTHVSQTQEQNKENQNPNSDAPVIRSKTSARYMELVGWLVDRGITSEK	240
5	NLAERKRLVAOHLTHVSOTOEONKENONPNSDAPVIRSKTSARYMELVGWLVDRGITSEK	,240
6	NLTERKRLVAQHLTHVSQTQEQNKENQNPNSDAPVIRSKTSARYMELVGWLVDXGITSEK	240
7	NLEERKRLVAQFLAESSQRS-QEAASQREFSADPVIKSKTSQKYMALVNWLVEHGITSEK	236
С	NL+ERKBLVA*+L***SQ***Q***+****S**PVI*SKTS**YM*LV*WLV*+GITSEK	
	250 260 270 280 290 · 300	
1	QWIQEDQASYISFNAASNSRSQIKAALDNAGKIMALTKSAPDYLVGPAPPADIKTNRIYR	300
2	QWIQEDQASYISFNAASNSRSQIKAALDNAGKIMALTKSAPDYLVGPAPPADIKTNRIYR	300
3	QWIQEDQASYISFNAASNSRSQIKAALDNASKIMSLTKTAPDYLVGSNPPEDITKNRIYQ	300
4	QWIQEDQASYISFNAASNSRSQIKAALDNASKIMSLTKTAPDYLVGSNPPEDITKNRIYQ	300
5	QWIQEDQASYISFNAASNSRSQIKAALDNASKIMSLTKTAPDYLVGQNPPEDISSNRIYR	300
6	QWIQEDQASYISFNAASNSRSQIKAALDNAGKIMSLTKTAPDYLVGQQPVEDISSNRIYK	300
7	QWIQENQESYLSFNSTGNSRSQIKAALDNATKIMSLTKSAVDYLVGSSVPEDISKNRIWQ	296
C	QWIQE *Q*SY*SFN***NSRSQIKAALDNA:KIM+LTK:A*DYLVG::**+DI::NRI*:	
	•	
_	310 320 330 340 350 360	
1	ILELNGYEPAYAGSVFLGWAQKRFGKRNTIWLFGPATTGKTNIAEAIAHAVPFYGCVNWT	360
2	ILELNGYDPAYAGSVFLGWAQKRFGKRNTIWLFGPATTGKTNTAEAIAHAVPFYGCVNWT	360
3	ILELNGYDPQYAASVFLGWAQKKFGKRNTIWLFGPATTGKTNIAEAIAHAVPFYGCVNWT	360
4	ILELNGYDPQYAASVFLGWAQKKFGKRNTIWLFGPATTGKTNTAEAIAHAVPFYGCVNWT	360
5	ILEMNGYDPQYAASVFLGWAQKKFGKRNTIWLFGPATTGKTNIAEAIAHAVPFYGCVNWT	360
6	ILELNGYDPQYAASVFLGWATKKFGKRNTIWLFGPATTGKTNIAEAIAHTVPFYGCVNWT	360
7	IFEMNGYDPAYAGSILYGWCQRSFNKRNTVWLYGPATTGKTNIAEAIAHTVPFYGCVNWT	356
С	I*E+NGY*P:YA:S***GW***:F*KRNT*WL*GPATTGKTNIAEAIAH+VPFYGCVNWT	

FIG. 3A

	370 380 390	400	410	2.0
٠,				20
1	NENFPFNDCVDKMVIWWEEGKMTAKVVESAKA	LLGGSKVRVDQKO	CKSSAQ <i>I</i> DPTPVIV	TS 420
2	NENF PFNDCVDKMVIWWEEGKMTAKVVESAKA	ILGGSKVRVDQKO	CKSSAQIDPTPVIV	TS 420
3	NENFPFNDCVDKMVIWWEEGKMTAKVVESAKA	ILGGSKVRVDQKO	KSSAQIEPTPVIV	TS 420
4	NENFPFNDCVDKMVIWWEEGKMTAKVVESAKA	ILGGSKVRVDOKO	KSSAOTEPTPVIV	TS 420
5	NENFPFNDCVDKMVIWWEEGKMTAKVVESAKA	ILGGSKVRVDOKO	KSSAOTDPTPVTV	TS 420
6	NENFPFNDCVDKMVIWWEEGKMTAKVVESAKA	TIGGSKVRVDOKO	Keesomproviv	TS 420
7	NENFPFNDCVDKMLIWWEEGKMTNKVVESAKA	TICCSMPMOY	VECTOTDETEVIV	TS 416
Ċ	NENFPFNDCVDKM*IWWEEGKMT*KVVESAKA	TICCEITEITECK	X35 VQIDSI PVIV	12 410
_				
٠,		460		80
1	NTNMCAVIDGNSTTFEHQQPLQDRMFKFELTR			
2	NTNMCAVIDGNSTTFEHQQPLQDRMFKFELTR	RLEHDFG <b>K</b> V <b>T</b> KQE	VKEFFRWAQDHVT	EV 480
3 -	NTNMCAVIDGNSTTFEHQQPLQDRMFKFELTR	RLDHDFGKVTKQE	VKDFFRWASDHVT	DV 480
4	NTNMCAVIDGNSTTFEHQQPLQDRMFKFELTR	RLDHDFGKVTKQE	VKDFFRWASDHVT	DV 480
5	NTNMCAVIDGNSTTFEHQQPLQDRMFKFELTK	RLEHDFGKVTKQE	VKDFFRWASDHVT	EV 480
6	NTNMCAVIDGNSTTFEHQQPLQDRMFKFELTR	RLDHDFGKVTKOE	VKDFFRWAKDHVV	EV 480
7	NTNMCVVVDGNSTTFEHQQPLEDRMFKFELTK	RLPPDFGKITKOF	VKDFFAWAKVNOV	PV 476
С	NTNMC * V * DGNSTTFEHQQPL * DRMFKFELT+	RI. *DEGK*TKOE	VKTEE*MV · * * * T	• ٧
		2101 1101	VICTLE WALL	• •
	490 500		510 5:	20
1	AHEFYVRKGGANKRPAPDDADKSEPKRA			
2	AHEFYVRKGGANKRPAPDDADKSEPKRA		-CPS VADPS TSDA	EG 522
	AMERIVANGGANARPAPUDADASEPARA		-CPSVADPSTSDA	EG 522
3	AHEFYVRKGGAKKRPASNDADVSEPKRQ			
4	AHEFYVRKGGAKKRPASNDADVSEPKRQ			
5	THEFYVRKGGARKRPAPNDADISEPKRA		-CPSVAQPSTSDAL	EA 522
6	EHEFYVKKGGAKKRPAPSDADISEPKRV			
7	THEFKVPRELAGTKGAEKSLKRPLGDVTNTSY	KSLEKRARLSFVP	ETPRSSDVTVDPA	PL 536
С	:HEF*V+***A:***A::***.*****:		+:*:*:*:**A	
				Ť
	530 540 550	560	570 58	30
1	APVDFADRYQNKCSRHAGMLQMLFPCKTCERM			
2	APVDFADRYQNKCSRHAGMLQMLFPCKTCERM	TOMENT CETUCTE		SQ 580
3	P-ADYADRYQNKCSRHVGMNLMLFPCKTCERM	OTCHTCE THEIR	DCSECT PT-GVSES	30 500
4	P ADVADENCE CONTINUE PORTOR OF THE CONTINUE P	NOTON VCL THEOR	DCGECT PGMSESQI	PV 581
	P-ADYADRYQNKCSRHVGMNLMLFPCKTCERM	NOISMACETHEOR	DCGECFPGMSESQI	PV 581
5	P-VDYADRYQNKCSRHVGMNLMLFPCRQCERM	NQNVDICFTHGVM	DCAECFP-VSESQI	PV 580
6	S-INYADRYQNKCSRHVGMNLMLFPCRQCERM			
7	RPLNWNSRYDCKCDYHAQFDNISNKCDECEYLI			
С	:::+:**RY**KC**H:**::****C::CE**1	7*::*:C**H*::	*C.*C**::+::	::
	590 600 610	620		
1	PVVRKRTYRKLCAIHHLLGRAPEIACSACDLVN	VDLDDCVSEO		623
2	PVVRKRTYRKLCAIHHLLGRAPEIACSACDLVN			623
3	SVVKKKTYOKLCPIHHILGRAPEIACSACDLAN			624
4	SVVKKKTYQKLCPIHHILGRAPEIACSACDLAN			624
5				
6	SVVRKRTYQKLCPIHHIMGRAPEVACSACELAN	ADT DDGT 225		623
	VSVVKKAYQKLCYIHHIMG-KVPDACTACDLVN			621
7	IPPWEKENLSDF	GUFDDANKEQ		610

FIG. 3B

-1-

SEQUENCE LISTING <110> Vega, Manuel Drittanti, Lila Flaux, Marjorie <120> MUTANT RECOMBINANT ADENO-ASSOCIATED VIRUSES <130> 37851-912PC <140> To Be Assigned <141> Herewith <150> 60/315,382 <151> 2001-08-27 <160> 735 <170> FastSEQ for Windows Version 4.0 <210> 1 <211> 621 <212> PRT <213> Artificial Sequence <223> Mutant rep protein: rep78 4 GCT <400>1

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Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
             260
                                265
                                                     270
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
         275
                            280
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290 295 300
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                     310
                                        315
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                 325
                                   330
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                               .. 345
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355
                            360
                                                365
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                        375
                                            380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                    390
                                       395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405
                                   410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
            420
                               425
                                                    430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
       435
                           440
                                                445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
    450
                        455
                                           460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                   470
                                       475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                485
                                   490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
           500
                               505
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
       515
                           520
                                               525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
    530
                       535
                                           540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                   550
                                      555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                565
                                   570
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580 585 590
                               585
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
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Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
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                       615
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-4-

Arg Leu Ala Arg Gly His Ser Leu <210> 3 <211> 621 <212> PRT <213> Artificial Sequence <223> Mutant rep protein: rep78 10 GCG <400> 3 Thr Ala Gly Phe Tyr Glu Ile Val Ile Ala Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 295 . Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg

-5-

390 395 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 415 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 495 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 510 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 520· 525 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 535 540 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 545 550 560 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 565 570 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 580 585 590 Ile His His Ile Met Gly Lys Val Fro Asp Ala Cys Thr Ala Cys Asp
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Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
             180
                                185
                                                     190
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
         195
                             200
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
     210
                         215
                                             220
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
                     230
                                        235
                                                            240
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245
                                    250
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
            260.
                                 265
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
        275
                            . 280
                                               285
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                        295
                                             300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                    310
                                        315
                                                             320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                    330
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
            340
                               345
                                                     350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355
                            360
                                                365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370
                        375
                                            380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405
                                   410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
       435
                           440
                                                445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450 455 460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                   470
                                       475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
               485
                                    490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
           500
                               505
                                                    510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
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Arg Leu Ala Arg Gly His Ser Leu
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- An

Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 50 55 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 150 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 · 185 190 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 270 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 295 . 300 . Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 350 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 390 395 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 415 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 445 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 505 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 520

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Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 

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-9-

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310
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                                  345
                                                       350
            340
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                             360
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 380
                                             380
                        375
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                          395
                    390
385
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                      410
                405
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                                       430
           420
                                 425
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                             440
       435
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
    450
                         455
                                             460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                          475
                    470
465
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
           500
                                 505
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515 520 525
Arg Leu Ala Arg Gly His Ser Leu
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Glu His Leu Pro Gly Ala Ser Asp Ser Phe Val Asn Trp Val Ala Glu
           20
                                 25
                                                       30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
                             40
        35
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                         55
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
```

90

170

110

140

155

Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 105

Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125

Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly

Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys

Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu

135

150

85

100

115

130

Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275. Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln . 455 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 580 590 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 

<sup>&</sup>lt;210> 8

<sup>&</sup>lt;211> 536 <212> PRT

<sup>&</sup>lt;213> Artificial Sequence

<220>
<223> Mutant rep protein: rep68 22 GCT

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ala Ser Asp Ser Phe Val Asn Trp Val Ala Glu Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 395 · Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 41.5 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln

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455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                        475
                  470
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                505
           500
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515 520 525
Arg Leu Ala Arg Gly His Ser Leu
<210> 9
<211> 621
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep78 29 GCG
Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
                                     10
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Ala Val Ala Glu
                                 25
            20
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
                            40
       35
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                        55
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                                   90
                85
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
100 105 110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115 120 125
       115
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
                        135
                                             140
  130
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145 150 155 160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
165 170 175
                165
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
180 185 190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
                            200
                                                  205
       195
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
                      215
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                     250
                245
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
260 265 270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                                                 285
       275
                            280
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290 295 300
                       295
                                             300
   290
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
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310

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Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                   330
                325
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                                                    350
                                345
            340
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                                            380
                       375
   370
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385 390 395 400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                    410
               405
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                425
            420
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                            440
        435
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450 455 460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                        475
                    470
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                                    510
                                505
            500
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                                                525
                           520
      515
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                      535
                                            540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                                       555
                    550
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                                    570
                565
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580 585 590
           580
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                                                605
                           600
       595
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                        615
  610
```

<sup>&</sup>lt;210> 10 <211> 536

<sup>&</sup>lt;212> PRT

<sup>&</sup>lt;213> Artificial Sequence

<sup>&</sup>lt;220>

<sup>&</sup>lt;223> Mutant rep protein: rep68 29 GCG

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105
           100
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
                                                 125
        115
                             120
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
                                         155
                   150
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
               165
                                     170
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
                             200
       195
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
                       215
  210
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245 250 255
                245
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 270
            260
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                                               285
                             280
        275
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                                             300
  290
                         295
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                   310
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                     330
                 325
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
            340
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                                              380
                        375
  370
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385 390 395 400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 410 415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                             440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                        455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 465 470 475 480
   450
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                  505
            500
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515 520 525
Arg Leu Ala Arg Gly His Ser Leu
    530
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<sup>&</sup>lt;210> 11

<sup>&</sup>lt;211> 621

<sup>&</sup>lt;212> PRT

<sup>&</sup>lt;213> Artificial Sequence

<220>
<223> Mutant rep protein: rep78 38 GCG

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu Lys Glu Trp Glu Leu Ala Pro Asp Ser Asp Met Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 145 150 155 160 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln

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455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                     470
                                           475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                                         510
            500
                                 505
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 525
        515
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 540
    530
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 545 550 560
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 565 570 575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580 585
                                  585
            580
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
595 600 605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
<210> 12
<211> 536
<212> PRT
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<213> Artificial Sequence

<220>
<223> Mutant rep protein: rep68 38 GCG

<400> 12 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 10 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 25 30 Lys Glu Trp Glu Leu Ala Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 45 40 35 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 110 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly 135 130 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys . 150 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 190 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 205 195 200 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 220 215 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 235 230

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 250 255 245 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 265 260 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285 280 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 300 295 290 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 310 315 320 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 350 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 390 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 415 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 425 430 420 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 440 435 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 460 450 455 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 495 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 510 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 Arg Leu Ala Arg Gly His Ser Leu 530

<210> 13

<211> 621

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep78 39 GCA

<400> 13 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 10 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 25 30 Lys Glu Trp Glu Leu Pro Ala Asp Ser Asp Met Asp Leu Asn Leu Ile 35 40 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 50 55 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 75 70 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile

105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 145 150 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 220 215 210 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 230 235 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 250 245 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 270 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 280 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 310 315 320 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 360 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430 420 425 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 445 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 475 470 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 495 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 505 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 525 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 535 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 545 550 560 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 565 570 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr

Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 595 600 605 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln

<210> 14

<211> 536

<212> PRT

<213> Artificial Sequence

<223> Mutant rep protein: rep68 39 GCA

<400> 14 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 25 30 Lys Glu Trp Glu Leu Pro Ala Asp Ser Asp Met Asp Leu Asn Leu Ile 35 40 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 50 55 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 105 100 110 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 150 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 190 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 230 235 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 270 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 285 275 280 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala

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Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 395 390 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 415 405 410 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 445 440 435 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465 470 475 475 470 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 495 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 520 515 Arg Leu Ala Arg Gly His Ser Leu 530

<210> 15 <211> 621 <212> PRT

<213> Artificial Sequence

<220>
<223> Mutant rep protein: rep78 53 GCT

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 25 30 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 45 40 Glu Gln Ala Pro Ala Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 95 90 85 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 105 100 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 120 125 115 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 155 150 145 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 170 165 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 190 185 180 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 200 205 195 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 220 215 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 235

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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                     250
                245
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                                                      270
            260
                                 265
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                            280
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290 295 300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                         315
                   310
305
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                                 345
            340
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                                             380
    370
                       375
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                         395
                     390
385
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                     410
                405
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
           420
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
435
440
445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450 455 460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465 470 475 480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                 505
           500
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                           520
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 535 540
       515
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 545 550 555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 565 570 575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
                                                       590
                                 585
           580
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                            600
        595
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
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<210> 16 <211> 536

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep68 53 GCT

Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 40 Glu Gln Ala Pro Ala Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 105 100 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 125 115 120 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 140 135 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 145 150 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 165 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 185 180 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 200 205 195 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 265 260 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
435
440
445 435 440 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 465 470 475 480 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 495 485 490 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val

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Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 525

Arg Leu Ala Arg Gly His Ser Leu 530 535

<210> 17 <211> 621 <212> PRT

<213> Artificial Sequence

<220>
<223> Mutant rep protein: rep78 59 GCG

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115

Pro Asn Tro Phe Ala Wal Tro Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 145 150 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 190 185 180 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 1.95 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 220 215 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 230 235 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 285 275 280 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 310 315 320 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 350 340 345 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala

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Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                   390
                                        395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 415
                                    410
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
            420
                                425
                                                    430
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435
                            440
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
    450
                       455
                                           460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                   470
                                       475
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                485
                                    490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
            500
                                505
                                                    510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                           520
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
    530
                       535
                                            540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                    550
                                        555
                                                            560
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                565
                                   570
                                                        575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
           580
                               585
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                          600
                                               605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
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<210> 18
<211> 536
<212> PRT
<213> Artificial Sequence
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Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
            20
                                25
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
       35
                           40
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Ala Gln Arg Asp Phe Leu
                       55
                                           60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
                    70
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                85
                                   90
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
                               105
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115 120 125
                                               125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly
                       135
                                           140
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Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys

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Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
                                                         175
                                    170
                165
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
                                185
            180
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
                                               205
                            200
       195
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
                       215
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                                        255
                                   250
               245
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                                                     270
                                265
           260
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                            280
        275
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                                             300
                       295
  290
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                        315
                   310
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                                345
            340
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                            360
       355
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                                             380
                       375
    370
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385 390 395 400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 410 415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                425
           420
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
       435
                            440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450 - 455 460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                        475
                 470
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                505
                                                     510
           500
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                            520
      515
Arg Leu Ala Arg Gly His Ser Leu
                        535
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<210> 19

<211> 621

<212> PRT

<213> Artificial Sequence

220>

<223> Mutant rep protein: rep78 64 GCT

<400> 19
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Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu

Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 40 35 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Ala 55 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 75 70 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 90 85 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 105 100 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 120 115 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 145 150 150 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 185 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 205 200 195 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225 230 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 270 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 310 315 320 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 330 325 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
435 440 445 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450 455 460 455 450 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 465 470 475 480 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 490 485 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 505

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Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 525 520 515 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 540 535 530 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 550 555 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 570 565 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 585 580 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln

<210> 20

<211> 536 <212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep68 64 GCT

<400> 20 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 30 25 20 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 40 45 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Ala 60 55 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 110 105 100 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly 135 130 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 155 150 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 170 165 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 185 180 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 200 195 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 250 245 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 270 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 285 280 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu

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295
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                         315
                   310
305
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                   330
                325
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                        375
    370
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385 390 395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                   410
                405
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
430
420
425
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                            440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450 455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                         475
                 470
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
            500
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515 520 525
Arg Leu Ala Arg Gly His Ser Leu
    530
<210> 21
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<211> 621

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep78 74 GCG

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Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 190 180 185 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 220 210 215 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 250 245 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 285 275 280 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 315 310 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 360 365 355 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 375 · 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 415 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 425 420 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 495 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 520 525 515 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 540 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 550 555 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 565 570 575 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 585 580 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 595 600 605 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 615

<210> 22 <211> 536

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<212> PRT <213> Artificial Sequence <220>

<223> Mutant rep protein: rep68 74 GCG

<400> 22 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 10 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 25 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Ala Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 95 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 145 150 155 160 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 235 240 Gln Trp Ile Gin Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 250 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 270 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 310 315 320 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 330 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 345 350 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 415 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 425

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 495 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 505 510 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 Arg Leu Ala Arg Gly His Ser Leu 530

<210> 23

<211> 621

<212> PRT

<213> Artificial Sequence

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<223> Mutant rep protein: rep78 86 GCG

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290
                          295
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                      310
                                          315
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325
                                     330
                                                           335
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345
                                345
                                                    . 350
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
     370
                         375
                                             380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                    390
                                         395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 410 415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435
                             440
                                                  445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                         455
                                             460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465
                   470
                                         475
                                                              480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                 505
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                         535
                                              540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 545 550 555
                                        555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
565 570 575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580 585
                                585
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
       595
                            600
                                                  605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                         615
<210> 24
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<211> 536

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep68 86 GCG

<400> 24

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 25 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 40 45 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 70

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Gln Phe Glu Lys Gly Ala Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 150 155 160 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Prc Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
420 425 430 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 445 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 465 470 475 480 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515
520 Arg Leu Ala Arg Gly His Ser Leu 

<210> 25 <211> 621

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<212> PRT <213> Artificial Sequence <220> <223> Mutant rep protein: rep78 88 GCC <400> 25 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 25 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 40 45 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 50 **5**5 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 70 75 80 Gln Phe Glu Lys Gly Glu Ser Ala Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 150 155 160 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 190. Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225 230 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 265 270 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 295 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 310 315 320 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 350 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 415

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Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 445 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 510 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 525 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 535 540 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 545 550 555 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 565 570 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 580 590 585 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 595 600 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 610 615

<210> 26

<211> 536

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein:rep 68 88 GCC

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 10 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 25 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 40 45 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 50 55 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Ala Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 110 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 145 150 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 190 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr

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220
                          215
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 235 240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
250 255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
260 265 270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305 310 315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
325 330 335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
355 360 365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 465 470 475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
500 505 510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515 520 525
 Arg Leu Ala Arg Gly His Ser Leu
 <210> 27
 <211> 621
 <212> PRT
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<213> Artificial Sequence

<223> Mutant rep protein: rep 78 101 GCA

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1 5 10 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 25 20 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 40 45 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 60 55 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 70

Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Ala Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 105 110 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly 130 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 145 150 155 160 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 265 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 280 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 360 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 415 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 425 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 445 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 465 470 475 480 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 495 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 505 510 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 520 525 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 535 540 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 550 555 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu

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Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 590

Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 595

Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln Gln 615

<210> 28 <211> 536 <212> PRT <213> Artificial Sequence

<220> <223> Mutant rep protein: rep68 101 GCA

<400> 28 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 10 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 25 30 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 40 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 90 Thr Thr Gly Val Ala Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 110 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 145 150 155 160 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 285 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 310 315 320 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 330 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 345

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Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp Arg Leu Ala Arg Gly His Ser Leu 

<210> 29

<211> 621

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep78 124 GCC

<400> 29

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ala Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly 130 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr

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215
                                                 220
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245 250 255
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 270
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
         275
                               280
                                                   285
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290 295 300
                          295
                                               300
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305 310 315
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                 325
                                        330
                                                              335
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
              340
                                   345
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
355 360 365
                              360
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                         375
                                               380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385 390 395 400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                       410
                                                             415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
420 425 430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435
                              440
                                                    445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450 455 460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465 470 475 480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                                       490
                                                            495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
             500
                                  505
                                                        510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515 - 520 525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 540
                        535
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
545 550 555
                    550
                                         555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                                   570
                 565
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580 585 590
                                585
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
595 600 605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
   610
<210> 30
<211> 536
<212> PRT
<213> Artificial Sequence
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<223> Mutant rep protein: rep68 124 GCC

<400> 30

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ala Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465 470 480 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala

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485
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
            500
                                505
                                                     510
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
        515
                            520
 Arg Leu Ala Arg Gly His Ser Leu
    530
                         535
 <210> 31
 <211> 621
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep78 125 GCG
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Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
            20
                                25
                                                    30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
        35
                            40
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                        55
                                            60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
                    70
                                        75
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                                  - 90
                85
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
            100
                                105
                                                    110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Ala Pro Thr Leu
115 120 · 125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly
                                           140
                        135
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145
                    150
                                        155
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
               165
                                    170
                                                        175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
            180
                               185
                                                    190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
       195
                            200
                                               205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225
                    230
                                        235
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245
                                    250
                                                        255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
           260
                               265
                                                   270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
       275
                                              285
                           280
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
  290
                        295
                                           300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                   310
                                       315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
               325
                                   330
                                                        335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
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Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 390 395 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 415 410 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 425. 430 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 490 485 495 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 510 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 540 535 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 550 555 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 565 570. 575 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 580 585 590 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 595 600 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 610 615

<210> 32 <211> 536

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep68 125 GCG

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 25 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 40 45 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 70 75 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 110 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Ala Pro Thr Leu 115 120 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly

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```
130
                          135
                                               140
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
 145
                     150
                                        155
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
                165
                                      170
                                                            175
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
                                  185
                                                       190
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
         195
                             200
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
     210
                        215
                                             220
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235
                                        235
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245 250 255
                                      250
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
260 265 270
                                  265
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
        275
                            280
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290 295 300
                      · 295
                                              300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305 310 315 320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325
                                      330
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
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Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                             360
                                                 365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385 390 395 400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405
                                     410
                                                          415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
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Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
       435 -
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                                                445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450 455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 465 470 475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
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<212> PRT
<213> Artificial Sequence
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450 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala

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485 490 495 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 510 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 525 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 535 540 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 550 555 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 565 570 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 580 585 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 595 600 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 615

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-47-

Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 285 280 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 350 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 390 395 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 415 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 440 445 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 495 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 510 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 Arg Leu Ala Arg Gly His Ser Leu 530 535

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											140				
7	130	17- <b>1</b>	17-1	N	~1	135	П. г.	TIO	Dro	Asn	140	T.e.u	Len	Pro	Tare
145	пуѕ	val	vaı	ASD	150	Cys	TÄT	116	FIO	155	- 7 -	<u> u</u> cu	<u> </u>		160
Thr	Gln	Pro	Glu	Leu		Tro	Ala	Tro	Thr	Asn	Met	Glu	Gln	Tyr	
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr		Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195	_		_		200	_			<b>m</b> 1	205		3	
Pro		Ser	Asp	Ala	Pro		He	Arg	ser	Lys	220	Ser	ALA	Arg	TYE
Mak	210	T	77-7	C1	T	215	17 n T	7 cm	Tare	Gly		Thr	Ser	Glu	Taza
225	GIU	nea	vai	GLY	230	пеа	Val	rop	נעם	235	***				240
Gln	Trp	Ile	Gln	Glu	qeA	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser		Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
		_	260		_	_,		265		m	+	T7_ 7	270	<b>61</b> -	G3
Ile	Met		Leu	Thr	ьуs	Thr		PTO	Asp	Tyr	ьец	285	GIY	GIII	GIII
Dro	172]	275	Acn	Tla	Ser	Ser	280 Asn	Ara	Tle	Tyr	Lvs		Leu	Glu	Leu
FIG	290	GLU	rsp	110	JCI	295	*****	3		-1-	300				
Asn	Gly	Tyr	Asp	Pro	Gln		Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
	m1	<b>~</b> 1	<b>-</b>	325	<b>3</b>	<b>-</b> 1.	<b>31</b> -	~1	330	T1.	. ה ד ת	ui a	ጥኩሎ	335	Dro
inr	Thr	GIĀ	ьуs 340	inr	ASI	TTE	АТА	345	Ala	Ile	мта	птэ	350	Val	FIO
Phe	Tvr	Glv	Cvs	Va1	Asn	Tro	Thr	Asn	Glu	Asn	Phe	Pro		Asn	aaA
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
	Val	Val	Glu	Ser		Lys	Ala	Ile	Leu	Gly	GŢĀ	Ser	ьys	Val	Arg 400
385	) cm	GI'n	Larg	Crc	390	Car	Ser	71 a	Gln	395 Ile	Asn'	Pro	Thr	Pro	
Val	vaħ	GIII	цур	405	пуз	SCI	JCL	AIU	410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys		Val	Ile	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln		Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
	_	435	-	_	_	_	440		<b>5</b> 1	G1	T	445	mb	T	<b>C</b> 1 n
GIu	Leu	Thr	Arg	Arg	Leu	Asp 455	His	Asp	Pne	Gly'	цуs 460	vai	Inr	гур	GIII
Glu	450 Val	Lus	Asn	Phe	Phe		Tro	Ala	Lvs	Asp		Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
				485					490					495	
Pro	Ser	Asp		qaA	Ile	Ser	GLu	Pro	Lys	Arg	vaı	Arg	510	ser	var
Δ3 a	Gln	Dro	500	Thr	Sar	Aen	Δla	505	Δla	Ser	Tle	Asn		Ala	Asp
AIA	GTII	515	Ser	TILL	Ser	Ash	520	GIU	ALG	UC1	***	525	-1-		P
Arq	Tyr	Gln	Asn	Lys	Cys	Ser		His	Val	Gly	Met	Asn	Leu	Met	Leu
	530					535					540				
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
545					550					555					560
Phe	Thr	His	GIY		Lys	Asp	Cys	Leu		Cys	Pne	Pro	var	575	GIU
C	G1 m	Dwo	17-1	565	17-1	₹7 <b>-</b> 1	Larg	Tare	570	Tyr	Gl n	Tage	T.e.11		Tvr
SCT.	ببيدي	-10	580	Ser	val	A CTT	nyo	585	nza	-1-		-70	590	-70	-4-
Ile	His	His		Met	Gly	Lys	Val		Asp	Ala	Cys	Thr	Ala	Cys	Asp
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Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 445 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 510 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 Arg Leu Ala Arg Gly His Ser Leu 530

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  Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                      310
                                            315
  Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335
  Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                                   345
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  Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365
  Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
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  Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
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  Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
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  Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
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                                  425
                                                        430
  Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
435 440 445
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                          455
                                               460
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465 470 475 480
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
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                                  505
                                                        510
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515 520 525
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
530 540
                                               540
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                                          555
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 565 570 575
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
                                 585
                                                       590
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Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
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Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu

Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Ala Ala Gly Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp Arg Leu Ala Arg Gly His Ser Leu 

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PCT/IB02/04087

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100 105 110 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 155 Ala Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 170 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
180 185 190 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 230 235 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 250 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 265 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 280 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 285 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 350 360 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 375 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400 380 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val

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Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 495 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 525 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 535 540 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 545 550 555 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 565 570 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 585 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 595 600 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 610 615

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Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 10 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 25 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 40 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 50 55 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 110 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 150 155 Ala Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 185 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn

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200
                                                    205
  Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
                           215
                                               220
  Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
  225
                       230
                                           235
  Gin Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
  Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                                                            255
                                  265
                                                        270
  Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                               280
  Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                          295 .
                                               300
  Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                      310
                                           315
                                                                320
  Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
  Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
              340
                                  345
                                                       350
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365
                                                  365
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
370 375 380
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                    390
                                          395
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 410 415
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                  425
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                             440
                                                  445
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450 455 460
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465 470 475 480
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                                      490
                                                          495
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
            500
                                 505
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
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 Arg Leu Ala Arg Gly His Ser Leu
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Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
                                 25 ~--
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
                            40
                                                45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
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Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 110 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Ala Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 . 245 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 495 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys

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550
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                 565
                                   570
                                                           575
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
             580
                                 585
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
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                             600
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
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 <211> 536
 <212> PRT
 <213> Artificial Sequence
 <223> Mutant rep protein: rep68 163 GCT
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Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
                             40
                                                  45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                         55
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                 85
                                      90
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
                                105
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115 120 125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly
                         135
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
                     150
                                          155
Thr Gln Ala Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
165 170 175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
                                185
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
195 200 205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
                         215
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245
                                    250
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                                265
           260
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                         295
                                              300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                    310
                                          315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
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Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 365 355 360 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 415 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 425 430 420 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 . 440 445 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 455 460 450 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 475 465 470 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 505 510 500 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 Arg Leu Ala Arg Gly His Ser Leu 530 535

<210> 43

<211> 621 <212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep78 175 GCT

<400> 43

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Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 190 180 185 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn

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200
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
                       215
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225
                     230
                                        235
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                 250
              245
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
260 265 270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                            280
                                                  285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290 295 300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305
                   310
                                         315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                     330
                 325
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
            340
                                 345
                                                     350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
   370
                        375
                                             380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400
                390
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
420 425 430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                            440
       435
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                        455
                                             460
    450
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                 470
                                         475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                 505
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515 520 525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                       535
   530
                                             540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 545 550 555
                   550
                                        555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
565 570 575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580 590
                                585
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
       595
                            600
                                                 605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
   610
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<sup>. &</sup>lt;210> 44

<sup>&</sup>lt;211> 536 <212> PRT

<sup>&</sup>lt;213> Artificial Sequence

<sup>&</sup>lt;223> Mutant rep protein: rep68 175 GCT

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<400> 44 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 1 5 10 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 40 45 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 50 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 135 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 150 155 160 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Ala Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 185 180 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 245 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 - 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 310 315 320 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 350 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 360 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 415 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 425 420 430 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475

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Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485

Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
500

Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515

Arg Leu Ala Arg Gly His Ser Leu
535

<210> 45 <211> 621 <212> PRT <213> Artificial Sequence

<220>

<223> Mutant rep protein: rep78 193 GCG <400> 45 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 25 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 40 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 60 50 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly 130 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 150 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 170 165 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 185 190 Ala Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 205 195 200 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 250 255 245 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 315 310 320 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro

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Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365
                                                 365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                         375
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                     390
                                          395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405
                                    410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
420 425 430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435
                             440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 465 470 475 480
                    470
                                         475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
               485
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                             520
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                    550
                                         555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
565 570 575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580 585 590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
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Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
<210> 46
<211> 536
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<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep68 193 GCG

<400> 46 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 25 30Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 70 75 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu

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Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly
                         135
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
                    150
                                        155
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
               165
                                    170
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
180 185 190
Ala Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
        195
                            200
                                                205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
                        215
    210
                                            220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
                    230
                                       235
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                   250
              245
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
260 265 270
            260
                                265
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                            280
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
    290
                        295
                                             300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305
                   310
                                        315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 350
            340
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
355 360 365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370
                                            380
                        375
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385
                   390
                                       395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
               405
                                 410
                                                        415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435
                            440
                                                 445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
   450
                        455
                                            460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                       475
                 470
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
               485
                                    490
                                                        495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
           500
                                505
                                                    510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515 520 525
Arg Leu Ala Arg Gly His Ser Leu
   530
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<sup>&</sup>lt;210> 47

<sup>&</sup>lt;211> 621

<sup>&</sup>lt;212> PRT

<sup>&</sup>lt;213> Artificial Sequence

<sup>&</sup>lt;220>

<sup>&</sup>lt;223> Mutant rep protein: rep78 196 GCC

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<400> 47 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 10 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 25 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 40 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 50 55 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 150 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 190 Leu Thr His Ala Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 330 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 350 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400 390 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 415 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470

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Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 510 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 525 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 535 540 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 550 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 565 570 575 · · · · 575 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 580 585 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 595 600 605 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 615

<210> 48 <211> 536 <212> PRT <213> Artificial Sequence

<220>
<223> Mutant rep protein: rep68 196 GCC

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260

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265

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Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                              280
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                                                 285
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
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                         295
                                              300
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
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                     310
                                         315
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
            . 340
                                 345
                                                      350
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370
                        375
                                             380
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385 390 395 400
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
             420
                                 425
                                                      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
         435
                            440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450
460
                                            460
                        455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465 470 480
                  . 470
                                         475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
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                                505
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Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
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Arg Leu Ala Arg Gly His Ser Leu
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Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
        35
                            40
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                       55
                                            60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                85
                                    90
                                                         95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
            100
                                105
                                                    110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
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Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ala Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355.... Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 390 . Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 415 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 35 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 545 550 560 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln

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Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 425 430 420 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 440 435 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 510 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 Arg Leu Ala Arg Gly His Ser Leu 530 535

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<400> 52

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260

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265

270

30

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Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
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                             280
                                               285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                                             300
    290
                        295
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                         315
305
                    310
                                                             320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325
                                    330
                                                          335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
            340
                                345
                                                    350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365
                             360
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                        375
                                             380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                   390
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
               405
                                   410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435
                            440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450 455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                   470
                                        475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 510
                                                    510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
        515
                            520
                                                525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
    530
                        535
                                            540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 545 550 560
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
               565
                                  570
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
            580
                                585
                                                    590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
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Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
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Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu

25 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile

Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ala Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp Arg Leu Ala Arg Gly His Ser Leu

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530 535 <210> 53 <211> 621 <212> PRT <213> Artificial Sequence <220> <223> Mutant rep protein: rep78 228 GCG Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 10 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 25 30 20 25 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 40 45 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 50 55 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 110 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 145 150 155 160 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 170 175 165 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His .180 185 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 205 200 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 215 Met Glu Leu Ala Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 270 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 315 320 310 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 350 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 375 . 380 370 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 390 395

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Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 415 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 425 430 420 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 445 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 455 460 450 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 475. 470 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 495 485 490 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 510 . 500 505 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 525 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 540 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 550 555 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 570 565 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 585 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 600 595 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 610 615 <210> 54 <211> 397 <212> PRT <213> Artificial Sequence

<223> Mutant rep protein: rep52 228 GCG

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185
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Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
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                            200
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                        215
                                              220
   210
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                    230
                                         235
225
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
           260
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
        275
                            280
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                                             300
                        295
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 305 310 315 320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
325 330 335
                325
                                    330
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 340 345
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
355 360 365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
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                        375
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
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Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
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Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
                                                 45
                            40
       35
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                                             60
                       55
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 70 75 80
                                         75
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                                     90
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
            100
                                 105
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
                                                 125
       115
                            120
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 145 150 155 160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
                                     170
               165
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
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Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
                          200
                                               205
     195
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
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                                          220
                      215
Met Glu Leu Ala Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
                   230
                                      235
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                   250
               245
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                                                   270
                               265
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                           280
                                              285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                       295
                                           300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                       315
                   310
305
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                                       335
                                   330
               325
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                              345
                                                   350
            340
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                                           380
                       375
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                       395
                   390
385
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                                       415
               405
                                   410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                              425
                                                   430
           420
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
       435
                           440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                       455
                                          460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                   470
                                     475
465
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
               485
                                  490
                                                       495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
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Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
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Arg Leu Ala Arg Gly His Ser Leu
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<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep40 228 GCG

<400> 56

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                                     90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                               105
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                           120
                                                125
       115
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                        135
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                    150
                                        155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
               165
                                     170
                                                         175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
            180
                                185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195
                            200
                                                205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                        215
    210
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 235 240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
               245
                                    250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
       275
                           280
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                        295
   290
Arg Leu Ala Arg Gly His Ser Leu
305
                    310
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Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
20 25 30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
        35
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
   50
                        55
                                            60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65 70 80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                                   90
               85
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
            100
                                105
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115 120
      115
                                               125
                            120
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
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Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Ala Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 425 . Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 525 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 540 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln

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 <211> 397
 <212> PRT
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                 25
            20
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
        35
                             40
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                          55
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                 85
                                     90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100 105 110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115 120 125
                            120
                                                   125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                         135
                                              140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                     150
                                         155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                     1:70
                165
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180 185 190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 195 200 205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
    210
                         215
                                              220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 235 240
225
                    230
                                         235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                 245
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
        275
                             280
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
    290
                         295
                                              300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305
                    310
                                          315
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 325 330 335
                325
                                    330
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 340 345 350
                                 345
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 355 360 365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
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                                              380
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Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
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<210> 59

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<211> 536 <212> PRT <213> Artificial Sequence <223> Mutant rep protein: rep68 231 GCC Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 25 30 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 40 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 110 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 120 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 145 150 155 160 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 170 165 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 190 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 220 Met Glu Leu Val Gly Trp Ala Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 270 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 280 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 350 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 390 395 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser

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Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 440 435 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 490 485 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 505 500 510 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 Arg Leu Ala Arg Gly His Ser Leu <210> 60 <211> 312 <212> PRT <213> Artificial Sequence <220> <223> Mutant rep protein: rep40 231 GCC Met Glu Leu Val Gly Trp Ala Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 20 25 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 35 40 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 55 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 1-00 105 110 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 115 120 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 130 135 140 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala

 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val

 180
 185
 190

 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
 200
 205

 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe

150

165

210 215 220 Clu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 230 240 Clu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 255

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg

155

175

170

Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 260 265 270

Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val

75 280 28

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Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
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                                             300
Arg Leu Ala Arg Gly His Ser Leu
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                    310
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<211> 621
<212> PRT
<213> Artificial Sequence
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Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
            20
                                25
                                                     30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
       35
                            40
                                                45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
   50
                        55
                                            60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu.
                                   90
                                                        95
               85
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
100 105 110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
                            120
        115
                                               . 125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly
                        135
                                            140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
                   150
                                      155
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
                165
                                    170
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
180 185 190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
       195
                            200
                                                205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
                                           220
                       215
Met Glu Leu Val Gly Trp Leu Val Asp Ala Gly Ile Thr Ser Glu Lys
225 230 235
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245
                                    250
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                               265
                                                    270
           260
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
       275
                           280
                                               285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
  290
                       295
                                           300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305
                    310
                                        315
                                                            320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                   330
               325
                                                        335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
           340
                               345 .
                                                   350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                            360
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Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala

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370 . 375 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 395 390 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 415 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 . 425 430 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 440 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 495 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 525 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 535 -540 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 550 555 560 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 565 570 . 575 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 585 580 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 595 600 605 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 610 615

<210> 62

<211> 397

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep52 234 GCG

Met Glu Leu Val Gly Trp Leu Val Asp Ala Gly Ile Thr Ser Glu Lys 10 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 20 25 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 35 40 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55 60 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 85 90 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 100 105 110 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 120 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 130 135 140 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 150

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Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 170 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 185 190 180 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 205 195 200 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 225 220 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 230 235 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 250 245 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 260 265 270 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 275 280 285 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 290 295 300 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 310 315 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 325 330 335 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu . 345 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 355 360 365 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 370 375 380 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln

<210> 63 <211> 536

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep68 234 GCG

<400> 63 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 10 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 25 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 40 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 70 75 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 110 100 105 110 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 120 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 150 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu

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170
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
            180
                                 185
                                                      190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
         195
                              200
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
Met Glu Leu Val Gly Trp Leu Val Asp Ala Gly Ile Thr Ser Glu Lys
225
230
235
Glp Trp Ile Clr Gl
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245 250 255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
             260
                                 265
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
        275
                             280
                                                   285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
    290
                         295
                                              300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                   310
                                         315
                                                                320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335
                                     330
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
340 345 350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355
                              360
                                                   365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
   370
                         375
                                              380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385 390 395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 410 415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
420 430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435
                             440
                                                  445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                        455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 465 470 475 480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                 505
            500
                                                       510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
       515
                             520
Arg Leu Ala Arg Gly His Ser Leu
<210> 64
<211> 312
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<213> Artificial Sequence
<223> Mutant rep protein: rep40 234 GCG
Met Glu Leu Val Gly Trp Leu Val Asp Ala Gly Ile Thr Ser Glu Lys
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala

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Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                            40
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                85
                                     90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100
                                 105
                                                    110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
        115
                            120
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130
                        135
                                             140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                    150
                                         155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
               165
                                   170
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180 185 190
           180
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195
                            200
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                        215
                                            220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                    230
                                       235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                245
                                   250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
        275
                            280
                                                285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
  290
                        295
                                          300
Arg Leu Ala Arg Gly His Ser Leu
                    310
<210> 65
<211> 621
<212> PRT
<213> Artificial Sequence
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<220>

<223> Mutant rep protein: rep78 237 GCC

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Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Ala Ser Glu Lys 225 230 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 310 320 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 465 470 480 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 540 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 545 550 560 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp

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Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                        615
 <210> 66
 <211> 397
 <212> PRT
 <213> Artificial Sequence
 <223> Mutant rep protein: rep52 237 GCC
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 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                 25
            20
                                                     30
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                            40
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
  50
                       55
                                            60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                85
                                     90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100
                                105
                                                     110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                          120
                                                125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130 135
Cys Val Asp Lys Met Val lle Trp Trp Glu Glu Gly Lys Met Thr Ala
                    150
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165
                                    170
                                                         175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
            180
                               185
                                                    190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
       195
                          200
                                               205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                                        235
                    230
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                    250
                245
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
           260
                               265
                                                   270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
275 280 285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
    290
                        295
                                            300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                   310
                                        315
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                325
                                    330
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
340 345 350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
355 360 365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                        375
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
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385 390 395 <210> 67 <211> 536 <212> PRT <213> Artificial Sequence <223> Mutant rep protein: rep68 237 GCC <400> 67 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 1.0 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 25 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 45 40 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 50 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 75 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 110 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 120 115 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 145 150 155 160 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 190 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Ala Ser Glu Lys 225 230 235 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 270 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 350 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 390 395

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Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 445 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 475 465 470 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val -500 505 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 Arg Leu Ala Arg Gly His Ser Leu 530

<210> 68 <211> 312 <212> PRT

<213> Artificial Sequence

<220>
<223> Mutant rep protein: rep40 237 GCC

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Ala Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 35 40 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 55 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 75 70 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 85 90 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 105 100 110 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 115 120 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 135 140 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 145 150 155 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 165 170 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 180 185 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 195 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 215 220 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 230 235 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 250 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala

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260
                                 265
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
275 280 285
        275
                         280
                                                285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
   290
                        295
                                             300
Arg Leu Ala Arg Gly His Ser Leu
                    310
<210> 69
<211> 621
<212> PRT
<213> Artificial Sequence
<220>
<223> Mutant rep protein: rep78 250 GCC
<400> 69
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Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
                                                    30
            20
                                25
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
        35
                            40
                                                45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                       55
                                           60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                85
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
            100
                                105
                                                    110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
       115
                           120
                                               125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly
                       135
                                          140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145 150 155 160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
               165
                                    170
                                                        175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
           180
                               . 185
                                                    190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
                           200
                                               205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
   210
                      215
                                           220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Ala Ile Ser Phe Asn Ala Ala
               245 -
                                   250
                                                        255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
           260
                               265
                                                    270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                         280
                                              285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
  290
                        295
                                           300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                   310
                                        315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
               325
                                   330
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                                345
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Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355
                            360
                                                 365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370.
                       375
                                             380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                       395
                  390
                                                             400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
               405
                                    410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                               425
           420
                                                     430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
       435
                            440
Glu Leu Thr Arg Arg Leu Asp Eis Asp Phe Gly Lys Val Thr Lys Gln
                       455
                                           460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                       475
                  470
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
            500
                               505
                                                    510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
       515
                           520
                                                525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
   530
                      535
                                            540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 545 550 555 560
                                       555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 565 570 575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
           580
                               585
                                                    590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
       595
                           600
                                                605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                        615
<210> 70
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<211> 397 <212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep52 250 GCC

<400> 70

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 10 Gln Trp Ile Gln Glu Asp Gln Ala Ser Ala Ile Ser Phe Asn Ala Ala 20 25 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 35 40 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 55 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80 70 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 100 105 110 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 115 120 125 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp

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```
135
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                 150
                                      155
145
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                  170
                                                       175
               165
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                               185
           180
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                               205
                           200
       195
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                                           220
                       215
  210
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                   230
                                      235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245 250 255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
           260
                               265
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                            280
       275
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                                           300
   290
                      295
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                   310
                                      315
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
325 330 335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                               345
           340
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
                            360
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                                           380
                       375
  370
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385
                    390
<210> 71
<211> 536
<212> PRT
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<213> Artificial Sequence

:220>

<223> Mutant rep protein: rep68 250 GCC

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 10 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 25 20 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 40 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 60 50 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 90 85 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 105 100 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 125 115 120 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly 130

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Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145
                    150
                                        155
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
                                    170
               165
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
                               185
                                                    190
           180
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
                            200
        195
                                                205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
                       215
                                            220
    210
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
                    230
                                        235
Gln Trp Ile Gln Glu Asp Gln Ala Ser Ala Ile Ser Phe Asn Ala Ala
245 250 255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
           260
                               265
                                                    270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
        275
                            280
                                                285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
    290
                                            300
                        295
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                   310
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                   330
              325
                                                        335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
           340
                               345
                                                    350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355
                            360
                                                365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                                           380
   370
                       375
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                  390
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 415
               405
                                  410
                                                      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
           420
                               425
                                                   430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435
                           440
                                               445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
   450
                       455
                                           460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                 470
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
               485
                                   490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
           500
                               505
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
       515
                           520
Arg Leu Ala Arg Gly His Ser Leu
   530
<210> 72
<211> 312
<212> PRT
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<213> Artificial Sequence

<223> Mutant rep protein: rep40 250 GCC

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys

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Gln Trp Ile Gln Glu Asp Gln Ala Ser Ala Ile Ser Phe Asn Ala Ala
                                 25
            20
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
35 40 45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                                               60
                         55
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80
                    70
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
85 90 95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100 105 110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115 120 125
                             120
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                                               140
   130
                          135
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                    150
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165 170 175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
            180
                                  185
                                                     190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195 200 205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
    210
                         215
                                               220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 235 240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245 250 255
                 245
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
        275
                             280
                                                   285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                         295
Arg Leu Ala Arg Gly His Ser Leu
                     310
<210> 73
<211> 621
<212> PRT
<213> Artificial Sequence
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<220>
<223> Mutant rep protein: rep78 258 GCC

<400> 73
Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 1
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 25
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 50
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Glu Val Clu Val Glu Val Clu Val Glu Val Clu Val Cl

Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 170 165 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 · 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 Ser Ala Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 270 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 345 350 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 390 395 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 415 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 425 430 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450
460 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 465 470 475 480 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 490 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 505 500 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 520 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 540 535 540 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 545 550 555 555 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 570 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr

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580
                                   585
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
         595
                             600
                                                   605
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                          615
 <210> 74
 <211> 397
 <212> PRT
 <213> Artificial Sequence
 <223> Mutant rep protein: rep52 258 GCC
 <400> 74
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
            20
Ser Ala Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 35 40
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                        55
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65 70 75 80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                 85
                                      90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                  105
                                                       110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115 120 125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130 135 140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                   150
                                        155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                 165
                                      170
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180 185 190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195
                             200
                                                  205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                        215
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225 230 235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                 245
                                      250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
        275
                            280
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290 295 300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 305 310 315 320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                325
                                     330
                                                           335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
            340
                                 345
                                                      350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
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Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                        375
  370
                                          380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385
                    390
<210> 75
<211> 536
 <212> PRT
<213> Artificial Sequence
<220>
<223> Mutant rep protein: rep68 258 GCC
Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
                                    10
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
                               25
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
        35
                           40
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                        55
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
                    70
                                        75
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
               85
                                   90
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
                               105
           100
                                                   110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
        115
                           120
                                               125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly
                        135
                                           140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145
                                       155
                    150
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
               165
                                  170
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
           180
                              185
                                                  190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
195 200 205
                           200
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
                       215
                                          220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
                   230
                                      235
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245 250 255
Ser Ala Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
           260
                                                   270
                               265
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
       275
                           280
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
   290
                       295
                                           300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305
                  310
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
              325
                                  330
                                                       335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                              345
                                                  350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                           360
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Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala

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375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 415 415 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430 425 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 465 470 475 480 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 490 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 510 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515 520 525 Arg Leu Ala Arg Gly His Ser Leu 530 535 <210> 76 <211> 312 <212> PRT <213> Artificial Sequence <223> Mutant rep protein: rep40 258 GCC <400> 76 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 10 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 20 25 Ser Ala Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 40 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55 60 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 85 90 90 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 120 125 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 145 150 155 160 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 165 170 175 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 180 185 190 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 195 200 205 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 215 220 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 230

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<210> 77 <211> 621 <212> PRT <213> Artificial Sequence

<220>

<223> Mutant rep protein: 78 260 GCG <400> 77 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 25 30 25 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 40 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 70 75 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 110 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 145 150 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 190 180 185 1901 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 Ser Asn Ser Ala Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala

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325
                                         330
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
             340
                                    345
                                                          350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
         355
                               360
                                                     365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
     370
                          375
                                                 380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385 390 395 400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 410 415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440.
                              440.
                                                     445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450
460
                         455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 465 470 475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
500 505 510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515 520 525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                         535
                                               . 540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 555 560
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 565 570 575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580 585 590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
       595
                             600
                                                    605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                          615
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<210> 78 - <211> 397 <212> PRT <213> Artificial Sequence

varas arciliciai sequence

<223> Mutant rep protein: rep52 260 GCG

<400> 78

 Met Glu Leu Val
 Gly Trp
 Leu Val
 Asp Lys
 Gly Ile
 Thr
 Ser
 Glu Lys

 Gln Trp
 Ile
 Gln Glu Asp Gln Ala
 Ser
 Tyr
 Ile
 Ser Phe Asn Ala
 Ala Ala Ala

 Ser
 Asn Ser
 Ala
 Ser Gln Ile
 Lys
 Ala
 Ala
 Leu Asp Asn Ala
 Gly Lys

 35
 40
 45
 45
 Ala
 Ile
 Met Ser
 Leu Thr
 Lys
 Thr
 Ala
 Pro
 Asp
 Tyr
 Leu Val
 Gly Gln Gln
 Gln
 Gln
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Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
       115
                           120
                                               125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130
                       135
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                   150
                                       155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
               165
                                   170
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
          180
                              185
                                                  190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195
                           200
                                               205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
    210
                       215
                                           220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                   230
                                      235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
               245
                                   250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                                                  270
           260
                               265
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
       275
                           280
                                               285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
   290
                                           300
                       295
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305
                   310
                                       315
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                                  330
               325
                                                       335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
           340
                               345
                                                   350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
                           360
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
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                                           380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385
                   390
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<210> 79

<211> 536

<212> PRT

<213> Artificial Sequence

<223> Mutant rep protein: rep68 260 GCG

<400> 79

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```
120
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly
                                          140
    130
                        135
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
                    150
                                        155
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
165 170 175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
            180
                                185
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
        195
                             200
                                                 205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
    210
                      215
                                            220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                     250
                245
Ser Asn Ser Ala Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
            260
                                 265
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
        275
                             280
                                                 285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290 295 300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 310 315 320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
              325
                                    330
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355
                             360
                                                 365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
  370
                       375
                                            380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 410
                                    410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
420 425 430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
       435
                            440
                                                 445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450
460
                                           460
                      455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 465 470 475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                485
                                    490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
            500
                                505
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
       515
                            520
Arg Leu Ala Arg Gly His Ser Leu
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                        535
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<210> 80

<211> 312 <212> PRT

<213> Artificial Sequence

<223> Mutant rep protein: rep40 260 GCG

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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
           20
                                25
                                                    30
Ser Asn Ser Ala Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
    50
                        55
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65
                    70
                                        75
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                    90
                85
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100
                                105
                                                    110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
        115
                            120
                                                125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130
                        135
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                    150
                                        155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
               165
                                    170
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
            180
                                185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195
                            200
                                                205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
    210
                       215
                                            220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                    230
                                       235
                                                            240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                   250
                245
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                                265
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
        275
                           280
                                                285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
  290
                       295
Arg Leu Ala Arg Gly His Ser Leu
305
                    310
<210> 81
<211> 621
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep78 263 GCC
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Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
                               25
                                                   30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
       35
                           40
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                       55
                                           60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
                   70
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Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ala Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 -Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 525 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu

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```
. 565
                                      570
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
            580
                                585
                                                     590
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
       595
                            600
                                                 605
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                         615
<210> 82
 <211> 397
 <212> PRT
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
            20
                                25
Ser Asn Ser Arg Ser Gln Ala Lys Ala Ala Leu Asp Asn Ala Gly Lys
       35
                            40
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
  50
                        55
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65 70 75 80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                85
                                     90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100
                               105
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115 120 125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                        135
                                             140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                    150
                                         155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165
                                     170
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180 185 190
           180
                               185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
       195
                           200
                                                205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225
                    230
                                        235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                   250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
       275
                            280
                                                 285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290 295 300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                    310
                                        315
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
               325
                                   330
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
340 345 350
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Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
        355
                          360
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                        375
                                            380
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
 385
                     390
 <210> 83
 <211> 536
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Mutant rep protein: rep68 263 GCC
 <400> 83
 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
                                     10
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
            20
                                25
                                                    30
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
        35
                             40
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
    50
                         55
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
85 90 95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
            100
                               105
                                                    110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115 120 125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135
                        135
                                            140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
                    150
                                        155
                                                             160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
                165
                                    170
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
            180
                               185
                                                    190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
       195
                            200
                                                 205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
    210
                        215
                                            220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                    250
               245
Ser Asn Ser Arg Ser Gln Ala Lys Ala Ala Leu Asp Asn Ala Gly Lys
260 265 270
                               265
                                                    270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
       275
                            280
                                               285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
    290
                        295
                                            300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                   310
                                        315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
325 330
                                  330
                                                        335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
            340
                                345
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Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp

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360
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 380
                                             380
                         375
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                     390
                                         395
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405
                                     410
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
420 425 430
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                             440
                                                  445
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
     450
                         455
                                             460
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                         475
                   470
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490
                                     490
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
            500
                                 505
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
       515
                             520
Arg Leu Ala Arg Gly His Ser Leu
<210> 84
<211> 312
<212> PRT
<213> Artificial Sequence
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<223> Mutant rep protein: rep40 263 GCC
<400> 84
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
           20
                                 25
Ser Asn Ser Arg Ser Gln Ala Lys Ala Ala Leu Asp Asn Ala Gly Lys
35 40 45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65 70 75 80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
90 95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100 105 110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                             120
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
   130
                        135
                                             140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                   150
                                        155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165 170 175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
           180
                                185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195
                            200
                                                 205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
```

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Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 230 235 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 260 265 270 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 275 280 285 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 290 295 Arg Leu Ala Arg Gly His Ser Leu 305 310 <210> 85 <211> 621 <212> PRT <213> Artificial Sequence <223> Mutant rep protein: rep78 264 GCG <400> 85 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 25 30 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 110 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 155 150 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 170 175 165 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His

185

Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 200

Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala

Ser Asn Ser Arg Ser Gln Ile Ala Ala Ala Leu Asp Asn Ala Gly Lys

Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu

Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala

280

265 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln

215

295

230

245

190

205

285

220

300

235

250

180

260

275

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310
                                          315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
              325
                                     330
                                                          335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                                 345
                                                      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                            360
                                                 365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370
                         375
                                             380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385
                    390
                                         395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                                          415
                405
                                     410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
420 425 430
           420
                                425
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                                                 445
                            440
        435
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                                             460
    450
                        455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 465 470 480
                    470
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 510
            500
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515 520 525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
530 540
                        535
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 545 550 550 560
                    550
                                        555
                                                               560
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                565
                                   570
                                                          575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580 585 590
           580
                                585
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
       595
                            600
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                         615
<210> 86
<211> 397
<212> PRT
<213> Artificial Sequence
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
           20
                                25
Ser Asn Ser Arg Ser Gln Ile Ala Ala Ala Leu Asp Asn Ala Gly Lys
      35
                            40
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                        55
                                             60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
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Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                             105
          100
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
       115
                           120
                                              125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                       135
                                           140
   130
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                   150
                                      155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
             165
                                  170
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                               185
           180
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                              205
       195
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                                           220
                       215
   210
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                                      235
                   230
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                  250
               245
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                           280
       275
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                                           300
   290
                     · 295
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                  310
                                       315
                                                           320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
325 330 335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                              345
                                                  350
           340
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
       355
                           360
                                              365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                       375
                                          380
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Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
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<210> 87
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<211> 536 <212> PRT

<213> Artificial Sequence

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<223> Mutant rep protein: rep68 264 GCG

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100
                                  105
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
       115
                             120
                                                 125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly
                       135
  130
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145 150 155 160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
                                     170
                165
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
                                185
                                                      190
            180
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
                            200
       195
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245 250 255
Ser Asn Ser Arg Ser Gln Ile Ala Ala Ala Leu Asp Asn Ala Gly Lys
            260
                                265
                                                      270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
       275
                          280
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
    290
                         295
                                             300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305
                    310
                                         315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335
                325
                                     330
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370
                        375
                                             380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                    390
                                         395
385
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
               405
                                    410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
420 425 430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
435
440
445
        435
                            440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450 455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                        475
                  470
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
               485
                                    490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 525
Arg Leu Ala Arg Gly His Ser Leu
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<210> 88
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<sup>&</sup>lt;211> 312

<sup>&</sup>lt;212> PRT

<sup>&</sup>lt;213> Artificial Sequence

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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                                    30
            20
                                25
Ser Asn Ser Arg Ser Gln Ile Ala Ala Ala Leu Asp Asn Ala Gly Lys
        35
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                                            60
   50
                        55
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                                        75
65
                    70
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
85 90 95
                                    90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100
                                105
                                                    110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                            120
                                                125
        1.15
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                                            140
    130
                        135
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                                        155
                                                             160
                  150
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                    170
                                                        175
                165
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                185
                                                    190
            180
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                                205
                            200
        195
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                        215
                                            220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                                       235
                    230
225
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                                        255
                245
                                   250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                                265
                                                    270
           260
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                                285
                            280
       275
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                       295
                                          - 300
 290
Arg Leu Ala Arg Gly His Ser Leu
305
                    310
<210> 89
<211> 621
<212> PRT
<213> Artificial Sequence
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Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
           20
                                25
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
                            40
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
```

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Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 150 155 160 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 220 -Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Ala Pro Ala 325 330 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 345 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 - 360 365 365 360 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 425 420 430 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 440 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 495 490 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 510 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu

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Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp . Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 

<210> 90 <211> 397 <212> PRT <213> Artificial Sequence

<220> <223> Mutant rep protein: rep52 334 GCG

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Ala Pro Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg · 165 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys

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325 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 340 345 350 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 355 360 365 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 375 380 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 385 390 395 <210> 91 <211> 536 <212> PRT <213> Artificial Sequence <223> Mutant rep protein: rep68 334 GCG <400> 91 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 10 15 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 40 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 145 150 160 150 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 190 180 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 270 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Ala Pro Ala 330

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Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 390 395 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 415 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435. 440 445 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 465 470 475 480 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 495 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 Arg Leu Ala Arg Gly His Ser Leu 535

<210> 92

<211> 312 <212> PRT

<213> Artificial Sequence

<223> Mutant rep protein: rep40 334 GCG

<400> 92

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 20 25 30 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 40 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55 60 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 75 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 90 85 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Ala Pro Ala 100 105 110 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 115 120 125 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 130 135 140 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 150 155 160 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 165 170 175 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser

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200
                                                  205
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
    210
                        215
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 235
                    230
                                      235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                     250
                245
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
        275
                                                 285
                            280
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                        295
  290
Arg Leu Ala Arg Gly His Ser Leu
305
                     310
<210> 93
<211> 621
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep78 335 GCT
Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
                                     10
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
                                 25
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
        35
                            40
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 50 60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
                    70
                                         75
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                85
                                     90
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
           100
                                105
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115 120 125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly
  130
                        135
                                           140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145 150 155 160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
                165
                                    170
                                                         175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
           180
                                185
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
195 200 205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
                        215
                                            220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225 230 235 240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
               245
                                    250
                                                         255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
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265

Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285

270

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Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                        295
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                       315
                   310
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Ala Ala
              325
                                  330
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                              345
           340
                                                   350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355
                           360
                                               365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370
                       375
                                           380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                  390
                                      395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
               405
                                  410
                                                      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
           420
                               425
                                                  430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435
                           440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                       455
                                          460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                 470
                                      475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
              485
                                  490
                                                      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
       515
                           520
                                              525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                      535
                                           540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                  550
                                     555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
               565
                                 570
                                                      575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
                               585
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
       595
                          600
                                              605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
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<210> 94 <211> 397 <212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep52 335 GCT

<400> 94

 Met Glu Leu Val
 Gly Trp Leu Val
 Asp Lys Gly Ile Thr Ser Glu Lys 1

 1
 5
 10
 15

 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 25
 30

 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 35
 40

 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50

 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu

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Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                  85
                                      90
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Ala Ala
             100
                                 105
                                                       110
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
        115
                            120
                                                   125
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
     130
                         135
                                               140
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                     150
                                          155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165 170 175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                  185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                              200
                                                   205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
    210
                         215
                                               220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                     230
                                         235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245 250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
        275
                             280
                                                   285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                         295
                                              300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 305 310 315 320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
325 330 335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 340 345 350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
355 360 365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
370 375 380
                                             380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
<210> 95
<211> 536
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<212> PRT

<213> Artificial Sequence

<223> Mutant rep protein: 68 335 GCT

<400> 95 Thr Ala Gly'Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 10 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 25 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 40 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val

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Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
150 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 185 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 235 230 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 310 315 320 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Ala Ala 325 330 335 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 445 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 495 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 510 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 525 Arg Leu Ala Arg Gly His Ser Leu 535

<210> 96 <211> 312

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<212> PRT
 <213> Artificial Sequence
 <223> Mutant rep protein: rep40 335 GCT
<400> 96
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
            20
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
        35
                             40
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
   50
                        55
                                             60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                    70
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                85
                                     90
                                                         95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Ala Ala
            100
                                 105
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115 120
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130
                        135
                                             140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                   150
                                        155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165
                                    170
                                                         175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
            180
                                185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                                 205
        195
                            200
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
    210
                       215
                                             220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                245
                                    250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
        275
                                                 285
                            280
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
  290
                        295
Arg Leu Ala Arg Gly His Ser Leu
                    310
<210> 97
<211> 621
<212> PRT
<213> Artificial Sequence
<220>
<223> Mutant rep protein: rep78 337 GCT
Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
                                    10
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
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Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 40 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 120 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly 130 135 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 150 155 160 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185. 190 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 230 235. Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 270 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 295 .300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 Ala Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  $\frac{340}{5}$  345 350 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 440 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 455 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485
490
495 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp

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520 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 535 540 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 550 555 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 565 570 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 585 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 595 600 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 610 <210> 98 <211> 397 <212> PRT <213> Artificial Sequence <220> <223> Mutant rep protein: rep52 337 GCT <400> 98 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 10 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 35 40 . 45 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55 60 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75. Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 85 90 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 105 100 Ala Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 115 120 125 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 135 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 150 155 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 165 170 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 180 185 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 195 200 205 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 215 220 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 235 240 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245

250

Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 260 265 270 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val

280 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp

245

275

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Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 355 360 365 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 

<210> 99 <211> 536 <212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep 68 337 GCT

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 

Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala

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310 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 Ala Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 350 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 390 395 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 495 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 510 505 510 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 Arg Leu Ala Arg Gly His Ser Leu 530 <210> 100 <211> 312 <212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep40 337 GCT

<400> 100 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 10 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 20 25 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 35 40 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 55 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 85 90 95 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 105 110 Ala Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 115 120 125 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 140 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 150 155 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg

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Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 180 185 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 200 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 215 220 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 230 235 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 265 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 280 285 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290 295 300 Arg Leu Ala Arg Gly His Ser Leu .310 <210> 101

<211> 621 <212> PRT

<213> Artificial Sequence

<220 >

<223> Mutant rep protein: rep 78 341 GCC

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 10 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 25 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 30 40 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 110 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 170 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 185 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 200 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 230 235 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 250

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265

270

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Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275
        275
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                         295
                                             300
   290
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                         315
                                                              320
                    310
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325
Thr Thr Gly Lys Ala Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                         375
   370
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                         395
                   390
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                                     430
                                425
            420
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435
                            440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450 455 460
                        455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                         475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                505
            500
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
       515
                            520
                                                 525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                                             540
                       535
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 545 550. 555
                   550.
                                         555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
565 570 575
               565
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580 585 590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                            600
       595
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                         615
<210> 102
<211> 397
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep52 341 GCC
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
                                     10
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                25
                                                     30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
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Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                          55
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                      70
                                         75
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
85 90 95
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
 Thr Thr Gly Lys Ala Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
         115
                             120
                                                 125
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                         135
                                             140
                     150
                                        155
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                                              160
                165
                                     170
                                                          175
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                 185
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                                    190
                                                205
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                         215
                                             220
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                    230
                                        235
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245 250 255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                        295
                                            300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                   310
                                        315
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                                                             320
               325
                                    330
                                                         335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
355 360 365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                       375
                                           380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                    390
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<sup>&</sup>lt;210> 103

<sup>&</sup>lt;211> 536

<sup>&</sup>lt;212> PRT

<sup>&</sup>lt;213> Artificial Sequence

<sup>&</sup>lt;220>

<sup>&</sup>lt;223> Mutant rep protein: rep68 341 GCC

<sup>&</sup>lt;400> 103

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 1 5 10 15 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 25 30 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 40 45 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu

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	50					55				_	60				
65	r Glu				70					75					80
Gli	n Phe	: Glu	Lys	Gly 85	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val 95	. Glu
Th	r Thr	Gly	Val		Ser	Met	Val	Leu 105		Arg	Phe	Leu	Ser		Ile
Arg	g Glu	Lys 115		Ile	Gln	Arg	Ile   120		Arg	Gly	Ile	Glu 125	Pro		Lev
Pro	Asn 130		Phe	Ala	. Val	Thr 135		Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
Asr 145	Lys	Val	Val	Asp	Glu 150		Tyr	Ile	Pro	Asn 155		Leu	Leu	Pro	Lys 160
Thi	Gln	Pro	· Glu	Leu 165		Trp	Ala	Trp	Thr 170		Met	Glu	Gln	Tyr 175	
	: Ala		180					185					190		
	1 Thr	195					200					205			
	Asn 210					215					220				
Met 225	: Glu	Leu	Val	Gly	Trp 230		Val	Asp	Lys	Gly 235	Ile	Thr	Ser	Glu	Lys 240
	Trp			245	_				250					255	
	Asn		260					265					270		_
	Met	275					280					285			
	Val 290					295					300				
305					310					315			•		320
	Lys			325			•		330					335	
	Thr		340					345					350		
	Tyr	355	-				360					365			
	Val 370					375					380				
385					390					395					400
	Asp			405					410					415	
	Val		420					425					430		
	Thr	435					440					445			
	Leu 450					455					460				
465	Val				470					475					480
	His			485					490					495	
	Ser		500					505					510		
	Gln	515					520	Glu	Ala	Ser	Ile	Asn 525	Tyr	Ala	qeA
Arg	Leu 530	Ala	Arg	Gly	His	Ser 535	Leu								

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<210> 104
 <211> 312
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Mutant rep protein: rep40 341 GCC
 <400> 104
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
                                     10
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
             20
                                 25
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                             40
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
     50
                         55
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                     70
                                         75
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                 85
                                     90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
             100
                                 105
                                                     110
 Thr Thr Gly Lys Ala Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                             120
                                                 125
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130
                         135
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                    150
                                        155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165
                                    170
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
            180
                                 185
                                                     190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195
                            200
                                                 205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
    210
                        215
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val
                245
                                    250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                                265
                                                     270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
        275
                            280
                                                285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                       295
                                            300
Arg Leu Ala Arg Gly His Ser Leu
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                    310
<210> 105
<211> 621
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep78 342 GCC
<400> 105
Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
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Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 75 70 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 Thr Thr Gly Lys Thr Ala Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 465 470 475 480 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val

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500
                                     505
                                                         . 510
   Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515 520 525
  Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 540
  Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                       550
                                           555
  Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 565 570 575
  Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580
585
590
  Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
  Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                            615
  <210> 106
  <211> 397
  <212> PRT
  <213> Artificial Sequence
 <223> Mutant rep protein: rep52 342 GCC
 <400> 106
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                                             15
                                  25
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                              40
                                                    45
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 60
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65 70 75 80
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                       90
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                   105
                                                       110
Thr Thr Gly Lys Thr Ala Ile Ala Glu Ala Ile Ala His Thr Val Pro
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 130
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
150 155 160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                                            175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                                      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 195 200 205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 215 220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225 230 235 240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245 250 255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
                                 265
                                                     270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
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Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 340 345 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 

<210> 107

<211> 536 <212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep68 342 GCC

<400> 107 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu

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295
                                             300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                        315
                    310
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325
                                    330
                                                         335
Thr Thr Gly Lys Thr Ala Ile Ala Glu Ala Ile Ala His Thr Val Pro
                                345
            340
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                                               365
                            360
        355
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                        375
                                            380
   370
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385 390 395 400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
               405
                                    410
                                                        415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435
                           440
                                                445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                       455
                                            460
   450
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                        475
                   470
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
              485
                                    490
                                                        495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
           500
                               505
                                                    510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                                                525
       515
                           520
Arg Leu Ala Arg Gly His Ser Leu
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<210> 108

<211> 312

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep40 342 GCC

<400> 108 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Ala Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala

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Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 165 170 175 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 180 185 190 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 195 200 205 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 215 220 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 230 235 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 250 255 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270 . 270 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 275 280 285 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 295 Arg Leu Ala Arg Gly His Ser Leu

<210> 109 <211> 621

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep78 347 GCA

<400> 109 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 25 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 40 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 70 75 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 95 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 145 150 155 160 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala

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250
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
             260
                                 265
                                                     270
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
         275
                            280
                                               285
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300
                                             300
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                    310
                                         315
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                 325
                                     330
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ala Ala His Thr Val Pro
             340
                                 345
                                                     350
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                             360
                                                 365
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370
                        375
                                             380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                     390
                                         395
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405
                                    410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
            420
                                425
                                                    430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
435
440
        435
                           440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
   450
                        455
                                            460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                        475
                     470
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                                    490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
        515
                           520
                                                525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
545 550 555
                    550
                                        555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
                565
                                   570
                                                       575
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
       595
                           600
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
   610
<210> 110
<211> 397
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep52 347 GCA
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Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala

10

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Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
     50
                         55
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65 70 75 80
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                 85
                                       90
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
             100
                                 105
                                                      110
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ala His Thr Val Pro
                             120
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 130
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145 150 155 160
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                     170
                                                           175
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
 The Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                             200
                                                   205
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
    210
                          215
                                               220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                     230
                                          235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245
255
                 245
                                     250
                                                          255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
        275
                             280
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 290 295 300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 305 310 315
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
325 330 335
                                                          335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 340 345 350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
                           360
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 370 380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385
                     390
<210> 111
<211> 536
<212> PRT
<213> Artificial Sequence
<220>
<223> Mutant rep protein: rep68 347 GCA
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Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 150 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 270 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
330
335 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ala Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 390 395 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 410 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 445 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 455 450 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 465 470 475 480 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp

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Arg Leu Ala Arg Gly His Ser Leu
 <210> 112
 <211> 312
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Mutant rep protein: rep40 347 GCA
 <400> 112
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
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 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
            20
                                 25
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
        35
                            40
                                                 45
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
    50
                         55
                                            60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                    70
                                        75
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                85
                                    90
                                                        95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100
                                105
                                                     110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ala Ala His Thr Val Pro
        115
                            120
                                                125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130
                        135
                                            140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145
                    150
                                        155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
               165
                                    170
                                                       175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
            180
                                185
                                                    190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195
                                                205
                            200
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
   210
                       215
                                            220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225
                    230
                                       235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                245
                                    250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
            260
                                265
                                                    270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
        275
                           280
                                                285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
  290
                        295
Arg Leu Ala Arg Gly His Ser Leu
                    310
<210> 113
<211> 621
<212> PRT
<213> Artificial Sequence
<220>
<223> Mutant rep protein: rep 78 350 AAT
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<400> 113 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 10 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 25 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 40 45 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 70 75 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 145 150 150 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 190 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
210
215
220 

 Met Glu Leu Val Gly Trp Leu Val Asp Lys
 Gly Ile Thr Ser Glu Lys

 225
 230
 235
 240

 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
 245
 250

 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 270 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 ´ 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Asn Val Pro 345 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 390 395 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val

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Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 510 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 520 525 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 540 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 550 555 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 570 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 580 585 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 595 600 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 610 615

<210> 114 <211> 397

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep52 350 AAT

<400> 114 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 10 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 20 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 35 40 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 85 90 90 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 100 105 110 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Asn Val Pro 115 120 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 130 135 140 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 145 150 155 160 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 165 170 175 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 185 190 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 200 205 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 215 220 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 235 240 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 250 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala

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260
                                   265
  Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
        275
                               280
                                                   285
  Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      290
                          295
                                               300
  Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
  305
                      310
                                           315
  Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                  325
                                      330
                                                           335
  Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                                 345
                                                      350
  Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
355 360 365
  Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                          375
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
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 <211> 536
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 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
            20
                                  25
                                                      30
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
         35
                              40
                                                  45
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                         55
                                             60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                ..85
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
100 105
                                 105
                                                      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115 120 125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
                    150
                                         155
                                                              160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
                165
                                     170
                                                          175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
           180
                                 185
                                                     190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
195 200 205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
   210
                       215
                                            220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 235 230 240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
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250

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 265

255

245

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Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
         275
                            280
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
    290
                        295
                                            300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                   310
                                        315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325
                                    330
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Asn Val Pro
            340
                                345
                                                    350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                            360
                                                365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370
                        375
                                           380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                   390
                                       395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
               405
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                425
                                                    430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435
                            440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
    450
                       455
                                           460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                  470
                                       475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485
                                   490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
           500
                               505
                                                    510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
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Arg Leu Ala Arg Gly His Ser Leu
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<210> 116

<211> 312 <212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep40 350 AAT

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135
                                             140
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                   150
                                      155
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165
                                    170
                                                         175
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
            180
                                 185
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195
                            200
                                                205
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
    210
                        215
                                            220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 235 230 235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245 250 255
                                    250
                                                        255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                                265
                                                    270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
        275
                          280
                                               285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
  290
                       295
                                            300
Arg Leu Ala Arg Gly His Ser Leu
                    310
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<223> Mutant rep protein: rep78 350 GCT
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Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
           20
                                25
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
       35
                          40
                                               45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 50 60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
                   70
                                       75
                                                            80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                                   90
                                                       95
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Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 110 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145 150 155 160 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 190 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 215

<400> 118

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Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
                     230
                                        235
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                 245
                                    250
                                                        255
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
            260
                                265
                                                    270
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
         275
                            280
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
    290
                         295
                                            300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305
                    310
                                        315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
               325
                                   330
                                                        335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
            340
                                345
                                                    350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365
                            360
                                                365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                        375
                                            380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385
                    390
                                        395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
               405
                                  410
                                                       415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
            420
                                425
                                                    430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435
                            440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                        455
                                           460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                    470
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
               485
                                    490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
           500
                               505
                                                    510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
        515
                            520
                                                525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
    530
                        535
                                            540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
545
                   550
                                       555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
               565
                                  570
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
            580
                               585
                                                   590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                           600
                                                605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
   610
                        615
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<212> PRT
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<223> Mutant rep protein: rep52 350 GCT
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Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys

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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                   25
  Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
35 40 45
  Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      50
                           55
  Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
85 90
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                   105
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
          115
                               120
                                                    125
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                           135
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                      150
                                          155
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                 165
                                      170
                                                             175
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180 185 190
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                              200
                                                   205
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
     210
                          215
                                                220
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225 230 235 240
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                 245
                                      250
                                                            255
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 260 265 270
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                              280
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
     290
                         295
                                              300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 305 310 315
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
325 330 335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 340 345 350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 355 360 365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                         375
                                              380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                     390
<210> 119
<211> 536 <212> PRT
<213> Artificial Sequence
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Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp

15
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500
                                   505
                                                         510
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515 520 525
  Arg Leu Ala Arg Gly His Ser Leu
     530
                           535
 <210> 120
 <211> 312
<212> PRT
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 Gin Trp Ile Gin Glu Asp Gin Ala Ser Tyr Ile Ser Phe Asn Ala Ala
            20
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                              4 Ō
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55 60
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                 85
                                      90 .
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100 105 110
                                  105
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val' Pro
                                                  125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                    150
                                         155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165
                                      170
                                                           175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                              200
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 215 220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 235 230 235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                245
                                     250
                                                          255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
        275
                            280
                                                285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290 295 300
Arg Leu Ala Arg Gly His Ser Leu
305
                     310
<210> 121
<211> 621
<212> PRT
<213> Artificial Seguence
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<220> <223> Mutant rep protein: rep78 354 GCC

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450 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 465 470 475 480 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 495 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 505 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515 520 525 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 540 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 545 550 560 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 565 570 575 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580 585 590 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 600 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln <210> 122 <211> 397 <212> PRT

<213> Artificial Sequence

<223> Mutant rep protein: rep52 354 GCC

<400> 122

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35 40 45 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
50
60 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 85 90 95 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 120 Phe Ala Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 130 140 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 145 150 155 160 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 170 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 195 200 205 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 215 220 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln

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Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 255 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 260 265 270 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 280 285 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 295 300 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 310 315 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 325 330 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 345 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 355 360 365 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp . 370 375 380 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 390

<210> 123

<211> 536 <212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep68 354 GCC

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245
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
            260
                                 265
                                                      270
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
         275
                             280
                                                  285
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                         295
                                              300
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
 305
                                         315
                    310
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
325 330
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
            340
                                 345
                                                      350
 Phe Ala Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
355 360 365
                             360
                                                  365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                        375
                                             380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385
                    390
                                         395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 415
                                   410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
            420
                                425
                                                     430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                             440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
   450
                        455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 465 470 475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
            500
                                505
                                                     510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                            520
Arg Leu Ala Arg Gly His Ser Leu
   530
<210> 124
<211> 312
<212> PRT
<213> Artificial Sequence
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<220> <223> Mutant rep protein: rep40 354 GCC

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Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Ala Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val Ala Gin Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp Arg Leu Ala Arg Gly His Ser Leu 

<210> 125

<211> 621

<212> PRT

<213> Artificial Sequence

<223> Mutant rep protein: rep78 363 GCC

<400> 125

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200
                                                  205
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 220
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245
                                     250
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
             260
                                265
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
         275
                            280
                                                285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
    290
                        295
                                             300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 310 315 320
                                         315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325
                                     330
                                                          335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
             340
                                 345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Ala Phe Pro Phe Asn Asp
         355
                             360
                                                 365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                       375
                                            380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385 390 395 400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405
                                    410
                                                         415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
420 425 430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435
                           440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                  470
                                        475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                485
                                     490
                                                         495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
            500
                                505
                                                     510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
       515
                           520
                                                525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                    550
                                        555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                565
                                     570
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580 585
                               585
                                                    590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
       595
                          600
                                                605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                        615
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<sup>&</sup>lt;210> 126

<sup>&</sup>lt;211> 397

<sup>&</sup>lt;212> PRT

<sup>&</sup>lt;213> Artificial Sequence

<sup>&</sup>lt;220>

<sup>&</sup>lt;223> Mutant rep protein: rep 52 363 GCC

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 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
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 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
              20
                                    25
                                                        30
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                              40
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
50 55
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65 70 75 80
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
85 90
                                       90
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                                        110
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115 120
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Ala Phe Pro Phe Asn Asp
     130
                          135
                                                140
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145 150 155 160
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                      170
                                                            175
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                              200
                                                    205
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                          215
                                                220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225 230 235 240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245 250 255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                             280
                                                    285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290 295 300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 305 310 315
                                          315
                                                                 320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 325 330 335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 340 345 350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
       355
                              360
                                                   365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 370 380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385
                     390
<210> 127
<211> 536
<212> PRT
<213> Artificial Sequence
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<220>

<223> Mutant rep protein: rep68 363 GCC

<400> 127

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Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 10 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 25 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 40 45 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 70 75 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 145 150 155 160 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 170 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 190 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 270 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 310 315 320 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Ala Phe Pro Phe Asn Asp 355 360 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 425 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala

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485
                                      490
                                                           495
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
             500
                                505
                                                      510
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
        515
                             520
                                                  525
 Arg Leu Ala Arg Gly His Ser Leu
 <210> 128
 <211> 312
 <212> PRT
 <213> Artificial Sequence
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                                      10
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
             20
                                 25
                                                     30
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
        35
                            40
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                     70
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                85
                                     90
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100
                                 105
                                                    110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115 120
                            120
                                                125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Ala Phe Pro Phe Asn Asp
130 135
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                    150
                                         155
                                                             160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
               165
                                    170
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195 200 205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 215 220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                    230
                                        235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                245
                                    250
                                                        255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
            260
                               265
                                                   270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
       275
                          280
                                                285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
 290
                        295
Arg Leu Ala Arg Gly His Ser Leu
305
<210> 129
<211> 621
<212> PRT
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<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep78 364 GCT

<400> 129 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 25 30 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 120 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 145 150 155 160 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 . 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 230 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 250 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 310 315 320 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 330 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 350 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Ala Pro Phe Asn Asp 355 360 365 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 375 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 390 395 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe

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435
                              440
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
     450
                       455
                                             460
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                   470
                                         475
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                 485
                                     490
                                                          495
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
             500
                                 505
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
         515
                            520
                                                 525
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 540
                                             540
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                     550
                                         555
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                 565
                                    570
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580 585
                                585
                                                    590
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                           600
                                                605
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
  610
                         615
 <210> 130
 <211> 397
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<223> Mutant rep protein: rep52 364 GCT
<400> 130
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
            20
                                25
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                            40
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55 60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65 70 75 80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
85 90 95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
           100
                               105
                                                    110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115 120 125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Ala Pro Phe Asn Asp
130 135
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                    150
                                       1.55
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
               165
                                   170
                                                         175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180 185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                           200
                                                205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
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Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 230 235 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 260 265 270 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 280 285 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 290 295 300 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 310 315 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 325 330 335 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 340 345 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 375 380 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 385 390

<210> 131 <211> 536 <212> PRT <213> Artificial Sequence

<220> <223> Mutant rep protein: rep68 364 GCT

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 10 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 25 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 40 45 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 70 75 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly 130 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 150 155 160 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 185 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 190 195 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys

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230
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
               245
                                      250
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
             260
                                  265
                                                       270
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                             280
                                                  285
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                        295
                                             300
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                     310
                                         315
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
325 330
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
340 345
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Ala Pro Phe Asn Asp
355 360 365
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
370 375 380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                     390
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 410 415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
            420
                                 425
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
435
440
        435
                           440
                                                  445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450 455 460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                    470
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
            500
                                505
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
       515
                            520
Arg Leu Ala Arg Gly His Ser Leu
   530
                         535
<210> 132
<211> 312
<212> PRT
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                                     IΩ
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
           20
                                 25
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                           40
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55 60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                                         75
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
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Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 100 105 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 115 120 125 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Ala Pro Phe Asn Asp 130 135 140 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 150 155 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 165 170 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 180 185 190 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 195 200 205 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 215 220 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 230 235 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 260 · 265 270 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 275 280 285 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 295 Arg Leu Ala Arg Gly His Ser Leu

<210> 133 <211> 621

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep78 367 GCC

<400> 133 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 25 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 40 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 75 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 110 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 150 155 160 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His

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180
                                  185
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
       195
                             200
                                                  205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255
                245
                                                          255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
            260
                                 265
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
        275.
                           280
                                             · 285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
  290
                                              300
                        295
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 310 315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
               325
                                     330
                                                           335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                                  345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Ala Asp 355 360 365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
  370
                         375
                                             380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385 390 395 400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 410 415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
420 425
            420
                                 425
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
       435
                                                 445
                           440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                        455
                                             460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 465 470 480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                485
                                     490
                                                          495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
           500
                                505
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515
520
                           520
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                        535
                                              540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 545 550 560
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                565
                                    570
                                                          575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580 589
           580
                                585
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
       595
                            600
                                                  605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                         615
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<sup>&</sup>lt;210> 134 <211> 397

<sup>&</sup>lt;212> PRT

<sup>&</sup>lt;213> Artificial Sequence

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 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
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 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
            20
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                             40
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
     50
                        55
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                 85
                                     90
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100
                                105
                                                     110
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
       115
                           120
                                                 125
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Ala Asp
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                     150
                                        155
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165
                                    170
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
       195
                            200
                                                 205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 215 220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                    230
                                       235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                245
                                    250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
        275
                            280
                                                 285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290 295 300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                   310
                                        315
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                325
                                   330
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                                345
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
355 360 365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                        375
                                           380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385
                    390
                                        395
<210> 135
<211> 536
<212> PRT
<213> Artificial Sequence
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<223> Mutant rep protein: rep68 367 GCC

<400> 135 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 40 45 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 50 55 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 150 155 160 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 190 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn . 195 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225 230 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 270 265 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  $\frac{340}{345}$  350 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Ala Asp 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 415 410 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 425 430 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 455

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Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 465 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 495 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 510 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 Arg Leu Ala Arg Gly His Ser Leu 535 <210> 136

<211> 312 <212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep40 367 GCC

<400> 136 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 10 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 20 30 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 40 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 55 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 75 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 85 90 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 100 105 110 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 120 125 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Ala Asp 130 135 140 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 155 150 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 165 170 175 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 180 185 190 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 195 200 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 215 220 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 235 240 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 265 270 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 275 280 285 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 290 295 300 Arg Leu Ala Arg Gly His Ser Leu 310

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<210> 137
  <211> 621
  <212> PRT
  <213> Artificial Sequence
  <223> Mutant rep protein: rep78 370 GCC
 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
                                    25
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
         35
                                40
                                                       45
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 50 55 60
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 75 70 80
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                  85
                                       90
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
100 105
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115 120 125
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145 150 155 160
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
                  165
                                        170
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
180 185
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
       195
                               200
                                                      205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
210

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225

230

230

240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245 250 255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
260 265 270
                                   265
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290 295 300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
325
330
335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
340
345
350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355
                               360
                                                     365
Cys Ala Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                          375
                                                380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                        410
```

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Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 445 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 495 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 505 510 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515 520 525 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 535 540 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 550 555 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 565 570 575 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 580 585 590 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 595 600 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 615

<210> 138 <211> 397 <212> PRT <213> Artificial Sequence

<220>

<400> 138

<223> Mutant rep protein: rep52 370 GCC

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 10 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 20 30 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 40 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55 60 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 85 90 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115
120
125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130
135
140

Cys Ala Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 145 150 155 160 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 180 185 190 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser WO 03/018820 PCT/IB02/04087

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195
                              200
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
     210
                         215
                                              220
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                     230
                                         235
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                245
                                    250
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
            260
                                 265
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
         275
                             280
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
    290
                        295
                                           . 300
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                    310
                                        315
                                                              320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 325 330 335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
             340
                                                      350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
355 360 365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
  370
                         375
                                            380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
<210> 139
<211> 536
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep68 370 GCC
<400> 139
Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
                                     10
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
20 25 30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
35 40
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
   50
                        55
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65 70 75 80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
               85
                                    90
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
                                105
                                                     110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
       115
                            120
                                                125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly
   130
                       135
                                          140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
                   150
                                       155
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
165 170 175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
           180
                                185
                                                    190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
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200

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Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
    210
                         215
                                              220
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
                     230
                                          235
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                      250
                 245
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
 260

Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
280

285
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                         295
                                             300
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                     310
                                         315
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                 325
                                     330
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                                345
                                                    350
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
355 360 365
Cys Ala Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                     390
                                         395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405
                                     410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
420 425 430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435
                            440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                        455
                                             460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                   470
                                        475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                485
                                    490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
            500
                               505
                                                     510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515 520 525
Arg Leu Ala Arg Gly His Ser Leu
   530
<210> 140
<211> 312
<212> PRT
<213> Artificial Sequence
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                25
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      35
                           .40
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                       55
                                            60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
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Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                 85
                                     90
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
             100
                                105
                                                     110
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                                             140
 Cys Ala Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                     150
                                         155
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                 165
                                    170
                                                         175
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
            180
                                 185
                                                    190
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                                 205
         195
                             200
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                         215
                                             220
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
 225
                     230
                                        235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
        275
                            280
                                                 285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
  290
                        295
Arg Leu Ala Arg Gly His Ser Leu
                     310
<210> 141
<211> 621
<212> PRT
<213> Artificial Sequence
<220>
<223> Mutant rep protein: rep78 376 GCG
<400> 141
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                                    10
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
           20
                                25
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
        35
                                                 45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                        55
                                            60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65
                   70
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
               85
                                   90
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
           100
                                105
                                                    110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115 120 125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
  130
                        135
                                            140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
                    150
                                        155
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Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 1.80 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 200 .. Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gin Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Ala Trp Glu Glu Gly Lys Met Thr Ala Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 525 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln

<sup>&</sup>lt;210> 142 <211> 397

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<212> PRT <213> Artificial Sequence <223> Mutant rep protein: rep 52 376 GCG <400> 142 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 10 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 20 25 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 35 40 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 55 60 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 85 90 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 100 105 110 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 115 120 125 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 130 135 140 Cys Val Asp Lys Met Val Ile Ala Trp Glu Glu Gly Lys Met Thr Ala 145 150 155 160 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 165 170 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 185 190 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 200 205 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 215 220 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 235 240 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 250 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 260 265 270 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 275 280 285 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 290 295 300 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 305 310 315 320 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 325 330 335 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 340 345 350 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 355 360 365 360 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 370 380 375 380 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 390 <210> 143 <211> 536

<sup>&</sup>lt;212> PRT

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<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep68 376 GCG

<400> 143 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala - 245 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys Met Val Ile Ala Trp Glu Glu Gly Lys Met Thr Ala Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe

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435
                              440
  Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
     450
                        455
                                            460
  Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
  465
                   470
                                         475
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485
490
495
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
             500
                                 505
                                                      510
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
         515
                            520
 Arg Leu Ala Arg Gly His Ser Leu
                          535
 <210> 144
 <211> 312
 <212> PRT
 <213> Artificial Sequence
 <223> Mutant rep protein: rep 40 376 GCG
 <400> 144
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
                                     10
                                                          15
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
             20
                                 25
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
        35
                            40
                                                 45
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65 70 75 80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                 85
                                     90
                                                         95
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100
                                105
                                                    110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
        115
                           120
                                                125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                         135
Cys Val Asp Lys Met Val Ile Ala Trp Glu Glu Gly Lys Met Thr Ala
145
                     150
                                        155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165
                                     170
                                                        175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
            180
                                185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195
                            200
                                                 205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
  210
                        215
                                            220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                    230
                                        235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                245
                                    250
                                                       255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
       275
                           280
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
```

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Arg Leu Ala Arg Gly His Ser Leu
 305
                     310
 <210> 145
 <211>. 621
 <212> PRT
 <213> Artificial Sequence
 <223> Mutant rep protein: rep 78 381 GCG
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                                     10
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
        35
                            40
                                                45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 50 60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
                     70
                                         75
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                85
                                    90
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
            100
                                 105
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
                            120
                                                125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly
                        135
                                            140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145 150 155 160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
                165
                                    170
                                                         175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
           180
                                185
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
       195 -
                           200
                                               205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
   210
                      215
                                           220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245
                                    250
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                               265
            260
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
        275
                           280
                                                285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
   290
                       295
                                            300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                   310
                                        315
                                                            320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
               325
                                   330
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                               345
                                                    350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
       355
                            360
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Ala Met Thr Ala
                        375
                                            380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
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390
                                            `395
                                                                   400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                 405
                                       410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
420 425 430
                                                         430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
435 440 445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                     470
                                            475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
500 505 510
            500
                                                        510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515 520 525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                         535
                                                540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 545 550 555
                                           555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 565 570 575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580 585
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
595 600 605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
 610
<211> 397
<212> PRT
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<210> 146

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep 52 381 GCG

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Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 

<210> 147

<211> 536 <212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep 68 381 GCG

<400> 147 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile · 100 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His

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Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
        195
                              200
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
     210
                         215
                                              220
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
                     230
                                         235
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
            260
                                 265
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                             280
                                                  285
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290 295 300
                         295
                                             300
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                    310
                                        315
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
             340
                                 345
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Ala Met Thr Ala
                         375
                                             380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385 390 395 400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 415
                                     410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
            420
                                 425
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                            440
                                                 445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                        455
                                            460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                   470
                                        475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
               485
                                     490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
            500
                                505
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
       515
                             520
Arg Leu Ala Arg Gly His Ser Leu
<210> 148
<211> 312
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep40 381 GCG
<400> 148
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
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Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 55 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 85 90 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 100 105 110 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 115 120 125 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp · 135 140 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Ala Met Thr Ala 150 155 160 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 165 170 175 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 180 185 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 195 200 205 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 215 220 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 230 235 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 250 245 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 260 265 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 275 280 285 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 290 295 Arg Leu Ala Arg Gly His Ser Leu 305 310

<210> 149 <211> 621 <212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep78 382 GCG

<400> 149 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 10 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 25 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 40 45 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 70 75 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 110 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly

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	13	0					13	5				14	0			
As 14	п Ly 5	s V	al '	Val	Ası	9 Gl 15	и Су 0	з Ту	r Il	e Pr	o As 15	n Ty:	r Le	u Le	u Pro	o Lys 160
Th	r Gl	n P	ro (	3lu	Let 169	ı Gl	n Tr	p Al	a Tr	p Th 17	r As	n Mei	t Gl	u Gl	n Ty:	r Leu
			]	L80	)				18	5				196	a Gli	n His
		1.5	95					20	0				209	u Ası 5	ı Glı	a Asn
	21	U					21.	5				220	)			y Tyr
. 22.	<b>o</b> '					230	)				23!	5				Lys 240
					245	i				250	0 .				259	Ala
			2	60					26	5				270	)	Lys
		27	/5					280	)				285	5		Gln
	290	J					295	5				300				Leu
305	•					310					315	5				Ala 320
					325					330	)	•			Pro 335	
			3	40					345	5				350	Val	
		35	5					360	)				365		Asn	
	370	,					375	,				380			Thr	
385						390					395				Val	400
					405					410					Pro 415	
			4.	20					425					430	Asn	
		43	5					440					445		Lys	
	450						455					460			Lys	
465						470					475				Glu	480
					485					490					Pro 495	
			50	0					505					510	Ser	
		212	•					520					525		Ala	
	530						535					540			Met	
242						550					555				Ile	560
					565					570					Ser 575	
			58	U					585					590	Cys	
		595						600					605	ALA	Cys	Asp
<b></b> u	610	UDII	va	<u>.</u> .	ap.		Asp 615	wsb	cys	тте	ьпе	Glu 620	GIN			

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<210> 150 <211> 397
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Mutant rep protein: rep 52 382 GCG
 <400> 150
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 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
            . 20
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
         35
                               40
                                                    45
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                          55
                                               60
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                     70
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
85 90
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100
                                   105
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                              120
                                                    125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 130 135 140

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Ala Thr Ala
                                          155
                      150
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165
                                       170
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
         195
                              200
                                                    205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 215 220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225 230 235 240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
            260
                                  265
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                              280
                                                    285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
    290
                         295
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 305 310 315 320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                 325
                                       330
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
            340
                                  345
                                                       350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
        355
                              360
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                         375
                                               380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                     390
                                           395
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<210> 151

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<211> 536
<212> PRT
<213> Artificial Sequence
<220>
<223> Mutant rep protein: rep 68 382 GCG
<400> 151

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Ala Thr Ala Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser

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Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435
                            440
                                                 445
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450 455 460
                        455
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                    470
                                         475
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                485
                                    490
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                505
            500
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 525
 Arg Leu Ala Arg Gly His Ser Leu
    530 ·
<210> 152
 <211> 312
 <212> PRT
 <213> Artificial Sequence
<220>
 <223> Mutant rep protein: rep40 382 GCG
<400> 152
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
           20
                                25
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                             40
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
    50
                        55
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65 70 75 80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                85
                                    90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100 105 110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                            120
                                                 125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                        135
                                            140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Ala Thr Ala
                    150
                                        155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
               165
                                   170
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
           180
                                185
                                                    190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
       195
                            200
                                                205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                        215
                                            220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                   230 .
                                       235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                245
                                   250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
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265

Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 280

270

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Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 290 295 Arg Leu Ala Arg Gly His Ser Leu <210> 153 <211> 621 <212> PRT <213> Artificial Sequence <220> <223> Mutant rep protein: rep78 389 GCG <400> 153 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 25 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 40 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 70 75 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly 130 135 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 145 150 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 190 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 230 235 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 250 245 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 310 315 320 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala

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375 Lys Val Val Glu Ala Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 415 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 445 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 505 500 510 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 525 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 535 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 545 550 555 560 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 565 570 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 585 590 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 595 600 605 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln

<210> 154

<211> 397

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep52 389 GCG

<400> 154

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 10 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 20 25 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 35 40 45 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55 60 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 85 90 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 100 105 110 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 115 120 125 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 130 135 140 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 150 155

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Lys Val Val Glu Ala Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 165 170 175 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 180 185 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 200 205 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 215 220 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 230 235 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 260 265 270 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 275 280 285 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 295 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 305 310 315 320 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 330 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 345 350 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 355 360 365 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 370 375 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 385 390

<210> 155

<211> 536

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep68 389 GCG

<400> 155 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 25 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 40 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 50 55 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 70 75 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu

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165
                                       170
                                                            175
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
             180
                                  185
                                                      190
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
        195
                              200
                                                  205
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
     210
                         215
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                     250
                 245
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
260 265 270
            . 260
                                 265
                                                      270
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
        275
                            280
                                                  285
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
     290.
                          295
                                              300
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                     310
                                          315
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
340 345 350
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365
                                                  365
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
370 375 380
Lys Val Val Glu Ala Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                     390
                                         395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
420 425 430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435
                             440·
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450 455 460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                    470
                                         475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                485
                                     490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
            500
                                505
                                                     510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 525
Arg Leu Ala Arg Gly His Ser Leu
    530
                         535
<210> 156
<211> 312
<212> PRT
<213> Artificial Sequence
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<223> Mutant rep protein: rep40 389 GCG
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
                                     10 .
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
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Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 35 40 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 55 60 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 75 70 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 100 105 110 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 120 125 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 130 135 140 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala Lys Val Val Glu Ala Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 165 170 175 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 180 185 190 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 195 200 205 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 215 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 230 235 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 260 265 270 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 280 285 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 290 295 300 Arg Leu Ala Arg Gly His Ser Leu 310

<210> 157

<211> 621

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep78 407 GCC

<400> 157

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 25 30 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 40 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 50 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu

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		119	5				120	)				125	5		
	130	)				135	5				140	)	a Gly	_	-
Asr 145		Val	l Val	l As <u>r</u>	Glu 150		туг	: Ile	Pro	Asr 155		Let	ı Leu	Pro	Lys 160
Thr	Glr	ı Pro	Glu	165		Tr	Ala	Tr	Thr 170		Met	Glı	ı Gln	Tyr 175	
Ser	Ala	су:	Let 180		Leu	Thr	Glu	185		Arg	Leu	. Val	. Ala 190	Gln	His
Leu	Thr	: His		. Ser	Gln	Thr	Glr 200		Gļn	Asn	Lys	Glu 205	Asn	Gln	Asn
	210	)				215	i	_		_	220		Ala	_	•
225					230					235			Ser		240
Gln	Trp	Ile	Gln	Glu 245		Gln	Ala	Ser	Tyr 250	Ile	Ser	Phe	Asn	Ala 255	
Ser	Asn	Ser	Arg 260		Gln	Ile	Lys	Ala 265		Leu	Asp	Asn	Ala 270	Gly	Lys
		275			_		280		_	_		285			
	290					295					300		Leu		
305					310					315			Gly	_	320
				325					330				Gly	335	
_			340					345					Thr 350		
		355	_			-	360					365	Phe		•
	370		•			375					380		Met -		
385					390					395			Lys		400
			-	405	_				410		-		Thr	415	
			420					425					Gly 430		
		435					440					445	Phe		
	450					455					460		Thr		
465					470					475			Val		480
				485					490				Arg	495	
			500					505					Glu 510		
		515					520					525	Tyr		
	530					535					540		Leu		
545					550					555			Asn		560
				565					570				Val	575	
			580					585					Leu 590		
тте	HIS	H15	тте	меt	GLY	ьys	Val 600	Pro	Asp	Ala	Cys	Thr 605	Ala	Cys	Asp

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Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
  <210> 158
  <211> 397
  <212> PRT
  <213> Artificial Sequence
 <223> Mutant rep protein: rep52 407 GCC
 <400> 158
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
        · 35
                             40
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                         55
                                            60
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65 70 75 80
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                 105
                                                      110
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
        115
                             120
                                                 125
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
     130
                        135
                                             140
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145 150 155 160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165
                                     170
                                                          175
Val Asp Gln Lys Cys Lys Ala Ser Ala Gln Ile Asp Pro Thr Pro Val
                                 185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195 -
                             200
                                                 205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                        215
                                             220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225 230 235 240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                245
                                     250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                                 265
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
        275
                           280
                                                285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                       295
                                             300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                    310
                                         315
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
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330

Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu

Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp

375 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln

345 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 360

340

335

365

-192-

385 390 395 <210> 159 <211> 536 <212> PRT <213> Artificial Sequence <220> <223> Mutant rep protein: rep68 407 GCC <400> 159 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 10 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 25 30 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 40 45 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 75 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 110 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 150 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 190 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 230 235 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 270 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 330 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 350 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 395

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Val Asp Gln Lys Cys Lys Ala Ser Ala Gln Ile Asp Pro Thr Pro Val 405 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 495 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 510 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 Arg Leu Ala Arg Gly His Ser Leu 535

<210> 160

<211> 312 <212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep40 407 GCC

<400> 160 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 10 15 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 20 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 35 40 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 85 90 95 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 100 105 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 115 120 125 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 130 135 140 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 150 155 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 165 170 175 Val Asp Gln Lys Cys Lys Ala Ser Ala Gln Ile Asp Pro Thr Pro Val 180 185 190 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 195 200 205 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 215 220 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 230 235 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala

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260 265 270 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 275 280 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 290 295 Arg Leu Ala Arg Gly His Ser Leu 305 310 <210> 161 <211> 621 <212> PRT <213> Artificial Sequence <223> Mutant rep protein: rep78 411 GCA <400> 161 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 10 15 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 25 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 40 45 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 145 150 155 160 145 150 155 160 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 190 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
275 280 285 280 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro

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Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355
                             360
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                         375
                                             380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385
                    390
                                         395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ala Asp Pro Thr Pro Val
405 410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
           420
                                425
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                            440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                        455
    450
                                            460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                        475
                    470
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
           500
                               505
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515 520 525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
530 540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 545 550 550
                   550
                                        555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
           580
                                585
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                            600
                                                 605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
  610
                        615
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<210> 162

<211> 397 <212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: 52 411 GCA

<400> 162 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 10 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 20 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 40 45 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 55 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 85 90 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 105 110 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 115 120 125 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp

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135 140 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 150 155 160 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 170 165 175 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ala Asp Pro Thr Pro Val 180 185 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 195 200 205 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 215 220 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 230 235 240 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 255 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 270 260 265 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 275 280 285 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 290 295 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 305 310 315 320 320 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 325 330 -Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 340 345 350 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 355 360 365 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 375 380 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 390 <210> 163 <211> 536 <212> PRT <213> Artificial Sequence <223> Mutant rep protein: 68 411 GCA <400> 163 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 25 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 40 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 60

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Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
                      150
                                          155
                                                              160
  Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
                  165
                                     170
  Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
             180
                                185
  Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
         195
                             200
                                                  205
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
                         215
                                             220
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 235 230
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                     250
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
            260
                                 265
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
         275
                             280
                                                285
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                         295
                                             300
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                    310
                                       315
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                 325
                                    330
                                                         335
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
             340
                                 345
                                                     350
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                             360
                                                 365
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370
                        375
                                           - 380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ala Asp Pro Thr Pro Val
                                    410
                                                         415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                425
                                                    430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435 -
                            440
                                                445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                        455
                                           460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                  470
                                       475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
               485
                                    490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                                   510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
       515
                           520
Arg Leu Ala Arg Gly His Ser Leu
   530
                        535
<210> 164
<211> 312
<212> PRT
<213> Artificial Sequence
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<220>

<223> Mutant rep protein: rep 40 411 GCA

<400> 164

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys

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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala

25

20

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```
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
  Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                           55
  Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80
  Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                   85
                                        90
  Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
              100
                                    105
                                                          110
  Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                               120
                                                      125
  Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 130 140

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                                            155
  Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165 170 175
  Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ala Asp Pro Thr Pro Val
                                    185
                                                         190
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 195 200 205
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                           215
                                                220
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                      230
                                           235
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 255
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 260 265 270
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                              280
                                                    285
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                           295
                                                300
 Arg Leu Ala Arg Gly His Ser Leu
 <210> 165
 <211> 621
 <212> PRT
 <213> Artificial Sequence
<223> Mutant rep protein: rep78 414 GCT
<400> 165
Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
                                       10
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
20 25 30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
        35
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                        55
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
                     70
                                          75
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                                       90
```

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Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly 135 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 185 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 200 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 235 230 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 270 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 285 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 330 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 345 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 360 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 365 375 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 380 390 395 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Ala Pro Val 405 410 415 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 425 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 440 445 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465 470 475 480 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
500 505 510 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 520 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 525 535 540 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 550 555 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 570 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr

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580 585 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 600 605 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 610 615 <210> 166 <211> 397 <212> PRT <213> Artificial Sequence <223> Mutant rep protein: rep52 414 GCT <400> 166 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 25 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 35 40 45 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55 60 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 85 90 95 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 100 105 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 130 135 140 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 150 155 160 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 165 170 175 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Ala Pro Val 185 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 200 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 215 220 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 235 230 235 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 255 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 260 265 270 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 280 285 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 290 295 300 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 305 310 315 320 315 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 325 330 335 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu

345

Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr

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Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 370 375 380

Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 395 395

<210> 167

<211> 536

<212> PRT <213> Artificial Sequence

<220>

<223> Mutant rep protein:rep68 414 GCT

<400> 167 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 25 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 45 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 150 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 190 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 230 235 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala - 245 250 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 270 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 345 350 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 360 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala

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375 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Ala Pro Val 405 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 410 415 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450
450 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465 470 480 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 490 495 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 Arg Leu Ala Arg Gly His Ser Leu 535 <210> 168 <211> 312 <212> PRT <213> Artificial Sequence <223> Mutant rep protein: rep40 414 GCT <400> 168 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 10 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 20 25 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys - 40 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55 60 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 70 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 85 90 95 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 100 105 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 115 120 125 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 130 135 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 155 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Ala Pro Val 180 185 190 185 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 200 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 215 220 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln

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Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 255 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 260 265 270 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 275 280 285 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 290 295 300 Arg Leu Ala Arg Gly His Ser Leu 305 310

<210> 169 <211> 621 <212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: 78 420 GCT

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 10 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 40 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 70 75 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu B5 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 110 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 145 150 155 160 145 150 155 160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 190 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 1.95 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 220 215 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 235 230 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 270 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala

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325
                                      330
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
             340
                                 345
                                                      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365
                                                  365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                         375
                                              380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                     390
                                         395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405
                                     410
                                                         415
Ile Val Thr Ala Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
420 425 430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
435
440
                             440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                    470
                                         475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                485
                                     490
                                                         495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
500 505 510
                                                      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                        535
                                             540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                    550
                                        555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 565 570 575
                                   570
                                                        57Ś
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
       595
                            600
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                        615
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<210> 170 <211> 397

<212> PRT <213> Artificial Sequence

<220>

<223> Mutant rep protein: rep 52 420 GCT

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 20 25 30 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 35 40 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55 55 60 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 85 90 95 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 105 110

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Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
        115
                            120
                                                125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                   150
                                       155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165
                                    170
                                                        175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
            180
                                185
                                                   190
Ile Val Thr Ala Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195
                           200
                                               205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                       215
                                           220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225
                    230
                                       235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                245
                                    250
                                                       255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
            260
                                265
                                                   270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
       275
                           280
                                               285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                       295
                                           300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305
                   310
                                       315
                                                           320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
               325
                                  .330
                                                       335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
           340
                              345
                                                   350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
                          360
       355
                                              365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
 370
                       375
                                          380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385
                   390
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<210> 171

<211> 536

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep68 420 GCT

<400> 171

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 10 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 40 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 75. Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 105 110 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu

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120
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly
     130
                         135
                                              140
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
                     150
                                         155
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
165 170 175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
            180
                                  185
                                                       190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
        195
                             200
                                                  205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
                                              220
                       215
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                 245
                                      250
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
             260
                                  265
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
        275
                             280
                                                 285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 310 315 320
                                         315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                     330
                                                           335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
             340
                                  345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                             360
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370
                       375
                                             380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385 390 395 400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405
                                     410
Ile Val Thr Ala Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
420 425 430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435
                            440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 465 470 475 480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
            500
                                505
                                                      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
       515
                            520
Arg Leu Ala Arg Gly His Ser Leu
<210> 172
<211> 312
<212> PRT
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<sup>&</sup>lt;213> Artificial Sequence

<sup>&</sup>lt;223> Mutant rep protein: rep40 420 GCT

# -207-

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<400> 172
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
                                     10
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
            20
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
        35
                             40
                                                 45
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                    70
                                         75
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                85
                                    90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100
                                105
                                                     110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
        115
                            120
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130
                        135
                                            140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                    150
                                        155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165
                                    170
                                                         175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
            180
                                185
                                                     190
Ile Val Thr Ala Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195
                            200
                                                205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 215 220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225
                    230
                                        235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                245
                                    250
                                                         255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
            260
                                                    270
                                265
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
        275
                           280
                                                285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
 290
                        295
                                            300
Arg Leu Ala Arg Gly His Ser Leu
305
                    310
<210> 173
<211> 621
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep78 421 GCC
<400> 173
Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
                                    10
                                                        15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
                                25
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
                            40
                                                45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                        55
                                            60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
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Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly 130 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 145 150 155 160 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 190 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 345 350 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 410 Ile Val Thr Ser Ala Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465 470 480 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 510 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 525 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 540 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 550 555 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu

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565
                                       570
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
             580
                                  585
                                                       590
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
         595
                             600
                                                  605
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                          615.
 <210> 174
 <211> 397
 <212> PRT
 <213> Artificial Sequence
 <223> Mutant rep protein: rep52 421 GCC
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 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
            20
                                  25
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                             40
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55 60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                 85
                                      90
                                                          95
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
             100
                                 105
                                                      110
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
        115
                            120
                                                  125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130 135 140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                     150
                                          155
                                                               160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165
                                     170
                                                          175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
            180
                                185
Ile Val Thr Ser Ala Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195 200 205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 215 220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                     230
                                          235
                                                               240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                 245
                                     250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
        275
                           280
                                                  285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290 295 300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 305 310 315
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                                   330
                325
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                                 345
```

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Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 355

Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 370 375

Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 385

<210> 175
<211> 536
<212> PRT
<213> Artificial Sequence

<220> <223> Mutant rep protein: rep68 421 GCC

<223> Mutant rep protein: rep68 421 GCC <400> 175 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp

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```
360
                                                   365
  Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
     370
                          375
                                              380
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385 390 395 400
  Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405
                                    410
 Ile Val Thr Ser Ala Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
          435
                             440
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
     450
                         455
                                              460
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                    470
                                         475
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                  505
                                                     510
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 525
 Arg Leu Ala Arg Gly His Ser Leu
                          535
 <210> 176
 <211> 312
 <212> PRT
 <213> Artificial Sequence
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 <223> Mutant rep protein: rep40 421 GCC
 <400> 176
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                                     10
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
            20
                                                     30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
        35 -
                             40
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55 60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65 70 75 80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
85 90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                105
                                                     110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                            120
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130
                        135
                                           140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                   150
                                        155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
               165
                                     170
                                                         175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                185
                                                    190
Ile Val Thr Ser Ala Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      . 195
```

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe

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Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 235 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 255 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 260 265 270 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 280 . 285 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 290 295 Arg Leu Ala Arg Gly His Ser Leu <210> 177

.<211> 621

<212> PRT

<213> Artificial Sequence

<223> Mutant rep protein: rep78 422 GCC

<400> 177 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 25 30 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 40 45 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 110 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 140 135 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 150 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 . 185 190 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 230 235 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 250 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 270 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 295 300 Asn Gly Tyr Asp . Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala

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```
310
                                          315
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                    330
                                                          335
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
340 345 350
                                                     350
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370
                        375
                                             380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385
                    390
                                         395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 415
Ile Val Thr Ser Asn Ala Asn Met Cys Ala Val Ile Asp Gly Asn Ser
420 425 430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                             440
                                                 445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                        455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                   470
                                        475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
500 505 510
                                505
                                                     510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                            520
                                                 525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
    530
                        535
                                             540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                    550
                                       555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
565 570 575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
           580
                                585
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
       595
                           600
                                                 605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                        615
<210> 178
<211> 397
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<212> PRT

<213> Artificial Sequence

<223> Mutant rep protein: rep52 422 GCC

<400> 178

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Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 100 105 110 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 115 120 125 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 135 140 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 150 155 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 165 170 175 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 180 185 Ile Val Thr Ser Asn Ala Asn Met Cys Ala Val Ile Asp Gly Asn Ser 195 200 205 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 215 220 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 230 235 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 255 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 260 265 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 275 280 285 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 290 295 300 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 310 315 320 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 325 330 335 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 340 345 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 355 360 365 365 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 375 380 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 385 390

<210> 179

<211> 536

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep68 422 GCC

<400> 179

# -215-

100 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125. 125. Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 145 150 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 190 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 235 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 390 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 415 Ile Val Thr Ser Asn Ala Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 495 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 510 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 Arg Leu Ala Arg Gly His Ser Leu

<sup>&</sup>lt;210> 180 <211> 312

<sup>&</sup>lt;212> PRT

<sup>&</sup>lt;213> Artificial Sequence

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<220>
 <223> Mutant rep protein: rep40 422 GCC
 <400> 180
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
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 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
            20
                                                     30
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
         35
                             40
                                                 45
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                         55
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                     70
                                         75
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                85
                                     90
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
             100
                                 105
                                                     110
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
         115
                             120
                                                 125
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130
                         135
                                            140
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                     150
                                        155
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165
                                     170
                                                        175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180 185 190
 Ile Val Thr Ser Asn Ala Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195
                            200
                                                205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                       215
    210
                                            220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225
                    230
                                        235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                245
                                    250
                                                        255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
            260
                                                    270
                                265
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
        275
                           280
                                               285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
   290
                       295
                                            300
Arg Leu Ala Arg Gly His Ser Leu
                    310
<210> 181
<211> 621
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep78 424 GCG
<400> 181
Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
                                    10
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
            20
                               25
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
```

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55 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 110 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 150 155 . Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 190 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 310 315 320 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 350 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 360 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 410 Ile Val Thr Ser Asn Thr Asn Ala Cys Ala Val Ile Asp Gly Asn Ser 420 425 430 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 440 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 495 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 510 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 535

275

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Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 550 555 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 565 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 580 585 590 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 595 600 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 615 <210> 182 <211× 397 <212> PRT <213> Artificial Sequence <223> Mutant rep protein: rep52 424 GCG Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 35 40 45 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55 60 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 85 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 100 105 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 115 120 125 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 130 135 140 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 145 150 155 160 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 165 170 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 180 185 Ile Val Thr Ser Asn Thr Asn Ala Cys Ala Val Ile Asp Gly Asn Ser 195 200 205 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 215 220 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 235 240 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245

250

300

Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val

Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu

Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys

280 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp

295

310

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330
                                                          335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                               345
                                                 350
            340
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
        355
                             360
                                                 365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                                            380
  370
                        375
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
<210> 183
<211> 536
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep68 424 GCG
<400> 183
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Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
                                 25
                                                     30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
        35
                            40
                                                 45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
   50
                        55
                                            60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
85 90 95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
            100
                                 105
                                                     110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
        115
                            120
                                                125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly
    130
                        135
                                             140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145 150 155 160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
                                    170
                                                         175
               165
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
            180
                                185
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
       195
                                                 205
                            200
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
  210
                        215
                                             220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
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Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys

Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu

Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala

Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala

Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln

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Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 350 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 390 395 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 415 405 410 415 Ile Val Thr Ser Asn Thr Asn Ala Cys Ala Val Ile Asp Gly Asn Ser 420 425 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 440 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 495 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 520 Arg Leu Ala Arg Gly His Ser Leu 530

<210> 184

<211> 312

<212> PRT

<213> Artificial Sequence

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<223> Mutant rep protein: rep40 424 GCG

<400> 184

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195
                                                    205
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 220
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
 225
                      230
                                           235
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245 250 255
                                     250
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
275 280 285
                                                  285
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                         295
 Arg Leu Ala Arg Gly His Ser Leu
 305
 <210> 185
 <211> 621
 <212> PRT
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 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
20 25 30
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
        35
                             40
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                         55
                                              60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
A5 90
                                     90
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
                                105
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115 120 125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly 130
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
                    150
                                         155
                                                              160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
                165
                                     170
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
      195
                             200
                                                 205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
                    230
                                       235
                                                             240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
               245
                                    250
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
260 265 270
                                265
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
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Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
   290
                        295
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                    310
                                       315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
               325
                                   330
                                                      335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
            340
                               345
                                                  350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355
                           360
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                       375
                                           380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                   390
                                       395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
               405
                                  410
                                                      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ala Asp Gly Asn Ser
                              425
           420
                                                  430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435
                           440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                       455
                                          460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                   470
                                      475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
              485
                                  490
                                                     495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
          500
                              505
                                                  510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
       515
                           520
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                      535
                                          540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                   550
                                      555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
               565
                                570
                                                    575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
          580
                              585
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                          600
                                              605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
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<210> 186 <211> 397

<212> PRT <213> Artificial Sequence

<220>

<223> Mutant rep protein: rep52 428 GCT

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                                    90
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Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100
                                 105
                                                      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                             120
                                                 125
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                         135
    130
                                             140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                   150
                                       155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165 170 175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180 185 190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ala Asp Gly Asn Ser
195 200 205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
               215
    210
                                            220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                 245
                                    250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
            260
                                 265
                                                     270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
        275
                            280
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
    290
                       295
                                            300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 305 310 315 320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 325 330 335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                               345
            340
                                                    350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
                           360
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 370 - 375 380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                    390
<210> 187
<211> 536
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep68 428 GCT
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Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ala Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp Arg Leu Ala Arg Gly His Ser Leu

<210> 188 <211> 312

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                                  25
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
         35
                             40
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                         55
                                             60
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65 70 75 80
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                 85
                                     90
                                                          95
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
             100
                                 105
                                                      110
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
        115
                           120
                                                 125
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 130
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                     150
                                         155
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
             180
                                185
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ala Asp Gly Asn Ser
        195
                            200
                                                 205
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 215 220
   210
                         215
                                             220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                     230
                                         235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                245
                                    250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                           280
                                                 285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
  290
                        295
Arg Leu Ala Arg Gly His Ser Leu
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<210> 189
<211> 621
<212> PRT
<213> Artificial Sequence
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<223> Mutant rep protein: rep78 429 GCC
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Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
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Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 40 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 105 110 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 150 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 190 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
210 215 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 270 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 350 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 390 395 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 415 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Ala Gly Asn Ser
420
425
430 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 440 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp

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520 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 540 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 550 555 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 565 570 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 585 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 595 600 605 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln <210> 190 <211> 397 <212> PRT <213> Artificial Sequence <220> <223> Mutant rep protein: rep52 429 GCC <400> 190 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 10 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 25 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 35 40 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 55 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 85 90 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 100 105 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 115 - 120 125 120 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 130 135 140 Cys Val Asp Lys Met Val The Trp Glu Glu Gly Lys Met Thr Ala 145 150 155 160 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 165 170 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 180 185 190 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Ala Gly Asn Ser 195 200 205 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 215 220 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 230 235 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 255 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 260 265 270

Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 280

Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 290 295 300

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Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 320

Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 335

Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 345

Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 355

Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 370

Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln Gln 395

<210> 191

<211> 536

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep68 429 GCC

<400> 191

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310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 350. Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 390 395 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Ala Gly Asn Ser 420 425 430 Thr Thr Phe-Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 440 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 495 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 Arg Leu Ala Arg Gly His Ser Leu <210> 192

<211> 312

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep40 429 GCC

<400> 192

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 20 25 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 35 40 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 55 60 Pro Val Glu Asp Ile Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 90 95 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 100 105 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 115 120 125 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 135 140 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 150 155 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 165 170

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Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 180 185 190 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Ala Gly Asn Ser 195 200 205 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 215 220 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 230 235 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 255 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 260 265 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 275 280 285 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 295 300 Arg Leu Ala Arg Gly His Ser Leu 310 <210> 193 <211> 621 <212> PRT <213> Artificial Sequence <220> <223> Mutant rep protein: rep78 438 GCG <400> 193 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 10 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 25 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 45 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 70 75 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 110 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 150 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 185 180 190 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala

250

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys

245

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 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                          280
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 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
    290
                         295 ·
                                             300
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                    310
                                         315
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325
                                     330
                                                          335
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
             340
                                 345
                                                      350
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
         355
                             360
                                                  365
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                                             380
                        375
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385 390 395 400
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 410 415
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                 425
                                                      430
 Thr Thr Phe Glu His Ala Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435
                            440
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450 455 460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                   470
                                        475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 .495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
            500
                                505
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Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 525
                            520
                                                 525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 540
                       535
                                            540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                    550
                                        555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                565
                                     570
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580
590
                                585
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
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                           600
                                                605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
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                         615
<210> 194
<211> 397
<212> PRT
<213> Artificial Sequence
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
            20
                                25
                                                     30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
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Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                        55
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                    70
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
               85
                                    90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
           100
                                 105
                                                     110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
        115
                           120
                                                125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130
                        135
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
               165
                                    170
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180 185 190
                                185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195
                            200
                                                205
Thr Thr Phe Glu His Ala Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
   210
                        215
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                   230
                                       235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
               245
                                   250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
       275
                           280
                                                285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
  290
                       295
                                           300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 305 310 315 320
                   310
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                325
                                    330
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
           340
                                345
                                                   350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
       355
                           360
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                       375
                                           380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
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<210> 195

<211> 536

<212> PRT

<213> Artificial Sequence

220>

<223> Mutant rep protein: rep68 438 GCG

<400> 195

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450
450 450 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465 470 480 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 495 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 510 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 520 Arg Leu Ala Arg Gly His Ser Leu

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<210> 196
 <211> 312
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Mutant rep protein: rep40 438 GCG
 <400> 196
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
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 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
            20
                                 25
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                             40
                                                 45
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
    50
                        55
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                    70
                                      · · 75
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                85
                                    90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100
                                 105
                                                     110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
        115
                            120
                                                 125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130
                        135
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                   150
                                       155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165
                                    170
                                                         175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
            180
                                185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195
                            200
                                                205
Thr Thr Phe Glu His Ala Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
    210
                        215
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                   230
                                       235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                245
                                    250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
        275
                            280
                                                285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
  290
                        295
Arg Leu Ala Arg Gly His Ser Leu
                    310
<210> 197
<211> 621
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep78 440 GCG
<400> 197
Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
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Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 25 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 40 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 150 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 415 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 Thr Thr Phe Glu His Gln Gln Ala Leu Gln Asp Arg Met Phe Lys Phe 440 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val

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Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
        515
                              520
                                                   525
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
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                        535
                                               540
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 545 550 560
                                         555
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                 565
                                      570
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580 585 590
            580
                                  585
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
       595.
                             600
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
   610
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 <213> Artificial Sequence
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
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Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
        35
                             40
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                        55
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
85 90 95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100
                                 105
                                                       110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
        115
                             120
                                                  125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130 135 140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145 150 155 160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165
                                      170
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                 185
            180
                                                      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195
                            200
                                                  205
Thr Thr Phe Glu His Gln Gln Ala Leu Gln Asp Arg Met Phe Lys Phe 210 215 . 220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 235 240
Glu Val Lys Asp Phe Phe Arg. Trp Ala Lys Asp His Val Val Glu Val 245 250 255
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Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala

Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val

265

270

260

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Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 

<210> 199

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<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep68 440 GCG

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130

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290
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 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305
                    310
                                           315
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                  325
                                      330
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
             340
                                  345
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                              360
         355
                                                 365
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
370 375
                                             380
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385 390 395 400
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405
                                      410
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
420 425 430
 Thr Thr Phe Glu His Gln Gln Ala Leu Gln Asp Arg Met Phe Lys Phe
                            440
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450 455 460
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 465 470 475 480
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                505
            500
                                                     510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 525
       515
Arg Leu Ala Arg Gly His Ser Leu
  530
                         535
<210> 200
<211> 312
<212> PRT
<213> Artificial Sequence
<223> Mutant -rep protein: rep40 440 GCG
<400> 200
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
            20
                                 25
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                            40
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
   50
                        55
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                85
                                     90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
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100 105 110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 120 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala

140

135

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Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 165 170 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 180 185 190 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 195 200 205 Thr Thr Phe Glu His Gln Gln Ala Leu Gln Asp Arg Met Phe Lys Phe 210 215 220 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 230 235 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245 250 255 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 260 265 270 . 260 265 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 275 280 285 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 290 295 300 Arg Leu Ala Arg Gly His Ser Leu 305

<210> 201

<211> 621

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep78 451 GCC

<400> 201

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 10 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 25 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 40 45 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 110 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 150 155 160 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 190 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 230 235 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala

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245
                                       250
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
              260
                                  265
                                                        270
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
         275
                              280
                                                  285
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290 295 300
                         295
                                              300
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                    310
                                           315
                                                                320
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
325 330 335
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
             340
                                  345
                                                      350
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
         355
                              360
                                                  365
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 380
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
 385
                      390
                                          395
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 415
                                                           415
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
            420
                                  425
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
445 445
Glu Leu Ala Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450 455 460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                   470
                                         475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
500 505 510
                                 505
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
        515
                           520
                                                 525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 545 550 555
                    550
                                          555
                                                               560
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                 565
                                     570
                                                          575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580 585
                                 585
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 595 600 605
                                                 605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
  610
                        615
<210> 202
<211> 397
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep52 451 GCC
<400> 202
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
                                     10
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
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Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
        35
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
    50
                        55
                                             60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                85
                                     90
                                                         95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100
                                 105
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
        115
                             120
                                                 125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130 135 140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                    150
                                       155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                    170
                165
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                 185
                                                     190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195
                            200
                                                 205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                       215
                                            220
Glu Leu Ala Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                   230
                                       235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                245
                                    250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
           260
                                265
                                                    270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
        275
                            280
                                                 285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
  290
                       295
                                            300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 305 310 315
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                325
                                    330
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
            340
                                345
                                                    350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
       355
                           360
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 370 375 380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                    390
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<sup>&</sup>lt;210> 203

<sup>&</sup>lt;211> 536

<sup>&</sup>lt;212> PRT

<sup>&</sup>lt;213> Artificial Sequence

<sup>&</sup>lt;220>

<sup>&</sup>lt;223> Mutant rep protein: rep68 451 GCC

<sup>&</sup>lt;400> 203

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp

1 5 10 15

Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
20 25 30

Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile

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Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 50 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 185 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 235 230 235 Gin Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 250 245 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 440 445 Glu Leu Ala Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 465 470 475 480 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 495 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 505 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp

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Arg Leu Ala Arg Gly His Ser Leu
 <210> 204
 <211> 312
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Mutant rep protein: rep40 451 GCC
 <400> 204
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
             20
                                 25
                                                     30
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
         35
                             40
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
     50
                         55
                                            60
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                 85
                                                         95
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100
                                 105
                                                     110
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
        115
                             120
                                                 125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                        135
                                             140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                    150
                                        155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165
                                     170
                                                         175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
            180
                                185
                                                    190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195
                            200
                                               205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 220
Glu Leu Ala Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                   230
                                        235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                245
                                    250
                                                        255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
           260
                               265
                                                   270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
        275
                          280
                                                285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
  290
                        295
                                            300
Arg Leu Ala Arg Gly His Ser Leu
<210> 205
<211> 621
<212> PRT
<213> Artificial Sequence
<220>
<223> Mutant rep protein: rep78 460 GCG
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<400> 205 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 155. Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu - 295 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 310 315 320 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 415 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Ala Val Thr Lys Gln Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 

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Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 510 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 525 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 535 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 550 555 545 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 565 570 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr -580 585 590 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 595 600 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 615

<210> 206 <211> 397

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep52 460 GCG

<400> 206 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 10 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 35 40 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 70 75 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 85 90 95 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 105 100 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 115 120 125 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 135 140 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 150 155 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 165 170 175 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 180 185 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 195 200 205 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 220 215 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Ala Val Thr Lys Gln 225 230 235 240 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 250 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala

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260
                                                         270
  Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
       . 275
                              280
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      290
                         295
                                              300
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305 310 315
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                  325
                                       330
                                                             335
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 340 345
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
                              360
                                                  365
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
   370
                          375
                                              380
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                      390
 <210> 207
 <211> 536
 <212> PRT
 <213> Artificial Sequence
 <220>
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 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
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 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
           20
                                  25
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
35 40 45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
50 60
                         55
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
100 105 110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115 120 125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly 130 140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
                     150
                                         155
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
165 170 175
                                      170
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
180 185 190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
                            200
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225 230 235 240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245
                                    250
                                                          255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
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Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 350 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Ala Val Thr Lys Gln 450 460 455 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 495 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 500 505 510 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 Arg Leu Ala Arg Gly His Ser Leu

<210> 208

<211> 312

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep40 460 GCG

<400> 208

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 25 20 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 35 40 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 55 60 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 85 90 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 100 105 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 120 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp

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135
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                    150
                                          155
                                                              160
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                 165
                                     170
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
             180
                                 185
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
    210
                        215
                                             220
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Ala Val Thr Lys Gln
                     230
                                         235
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 255
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
        275
                          280
                                                 285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290 295 · 300
                        295 ·
Arg Leu Ala Arg Gly His Ser Leu
 <210> 209
<211> 621
<212> PRT
 <213> Artificial Sequence
<220>
<223> Mutant rep protein: rep78 462 GCC
<400> 209
Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
                                    10
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
20 25 30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
       35
                            40
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
   50
                        55
                                            60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65 70 80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                85
                                   90
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
100 105 110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
       115
                            120
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
                    150
                                        155
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
                                  170
               165
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
           180
                               185
                                                    190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
    195
                            200
                                                205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
                        215
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Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
                     230
                                         235
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245
                                   250
                                                        255
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
            260
                                 265
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
         275
                             280
                                                285
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
    290
                        295
                                            300
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
 305
                     310
                                        315
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325
                                   330
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
            340
                                345
                                                     350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
         355
                            360
                                                365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370
                        375
                                            380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385
                   390
                                       395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405
                                    410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
            420
                                425
                                                    430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435
                            440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Ala Lys Gln
    450
                        455
                                            460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                    470
                                       475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
               485
                                   490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
            500
                                505
                                                    510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
        515
                           520
                                               525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
    530
                       535
                                            540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                   550
                                       555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                565
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
           580
                               585
                                                   590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
        595
                           600.
                                                605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
   610
                        615
<210> 210
<211> 397
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep52 462 GCC
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Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys

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10
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
             20
                                  25
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
35 40 45
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                  85
                                       90
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
             100
                                  105
                                                        110.
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115 120 125
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                          135
                                                140
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                                          155
                      150
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                      170
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180 185 190
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195 200 205
                                                   205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
    210
                          215
                                               220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Ala Lys Gln 225 230 235
                                          235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
        275
                            280
                                                  285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
  290
                         295
                                               300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                     310
                                          315
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 325 330 335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 340 345
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
355 360 365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                         375
                                               380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                     390
<210> 211
<211> 536
<212> PRT
<213> Artificial Sequence
<220>
<223> Mutant rep protein: rep68 462 GCC
<400> 211
Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1 10 15
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Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 25 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 70 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly 130 135 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 150 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 230 235 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 350 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 415 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Ala Lys Gln 450 455 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val

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 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
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 Arg Leu Ala Arg Gly His Ser Leu
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
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Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
        35
                             40
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65 70 75 80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100
                                 105
                                                      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
        115
                            120
                                                 125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                        135
                                            140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145 150 155 160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165
                                     170
                                                          175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
            T80
                                185
                                                     190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195
                            200
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Ala Lys Gln 225 230 235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                245
                                     250
                                                         255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
            260
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Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
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                          280
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Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
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Arg Leu Ala Arg Gly His Ser Leu
305
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<212> PRT
<213> Artificial Sequence
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<220>
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450
                          455
                                               460
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
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                                         475
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
                                                          495
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
            500
                                 505
                                                      510
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 525
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                        535
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                    550
                                         555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 565 570 575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
            580
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 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
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<211> 397
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
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Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
        35
                            40
                                                  45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55 60
                        55
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                85
                                     90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100 105 110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
       115
                             120
                                                 125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                        135
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145 150 155
                  150
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165
                                     170
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180 185 190
                                185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
       195
                           200
                                                 205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
  210
                       215
                                            220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Ile Lys Gln
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230

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Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 260 265 270 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 275 280 285 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 300 295 290
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
310
320 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 340 345 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 355 360 365 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 375 380 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 385 390 395

<210> 215

<211> 536

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<223> Mutant rep protein: rep68 462 ATA

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250
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
260 265 270
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                                                  285
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                          295
                                               300
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 310 315
                                          315
                                                                 320
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325
                                      330
                                                             335
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
              340
                                   345
                                                       350
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
     370
                         375
                                               380
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 445
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Ile Lys Gln
450 455 460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 465 470 480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
500 505 510
                                 505
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      51.5
                             520
                                                    525
Arg Leu Ala Arg Gly His Ser Leu
                          535
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
            20
                                  25
                                                    . 30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
       35
                            40
                                                  45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
50
55
60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65 70 75 80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                      90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                  105
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245

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Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Ile Lys Gln Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp Arg Leu Ala Arg Gly His Ser Leu 

<210> 217

<211> 621

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep78 484 GCC

<400> 217

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 145 150 155 160 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn

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200
                                                     205
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
     210
                      215
                                               220
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225
230
230
240
 Gin Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245 250 255
                 245
                                       250
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
              260
                                    265
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
         275
                              280
                                                  285
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290 295 300
                                                300
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 310 315
                                            315
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
              340
                                   345
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
         355
                              360
                                                   365
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 380
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385 390 395 400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 415
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                  425
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
435 440 445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450 455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                     470
                                          475
Glu His Glu Ala Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485
490
495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
500 505
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515 520 525
       515
                                                   525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 545 550 555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 565 570 575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580 585 590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
595 600 605
                            600
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
   610
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<sup>&</sup>lt;210> 218

<sup>&</sup>lt;211> 397 <212> PRT

<sup>&</sup>lt;213> Artificial Sequence

<sup>&</sup>lt;220>

<sup>&</sup>lt;223> Mutant rep protein: rep52 484 GCC

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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
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Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65 70 75 80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
85 90 95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100 105 110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115 120
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130
                         135
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                    150
                                         155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165 170 175
                165
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
            180
                                  185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                             200
                                                   205
        195
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                         215
                                              220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 235 240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 255
Glu His Glu Ala Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
        275
                             280
                                                   285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
    290
                         295
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 305 310 315 320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                 325
                                      330
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
340 345
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
       355
                             360
                                                  365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                         375
                                             380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385
                     390
<210> 219
<211> 536
<212> PRT
<213> Artificial Sequence
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<223> Mutant rep protein: rep68 484 GCC

<400> 219

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485
                                      490
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
            500
                                 505
                                                       510
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
        515
                              520
 Arg Leu Ala Arg Gly His Ser Leu
    530
 <210> 220
 <211> 312
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                 25
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
        35
                             40
                                                 45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                85
                                     90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 100 105 110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
        115
                             120
                                                 125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
  130
                       135
                                            140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145 150 155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165·
                                     170
                                                         175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180 185 190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
       195
                            200
                                                 205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 215 220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 235 240
                    230
                                        235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                245
                                    250
                                                         255
Glu His Glu Ala Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
           260
                                                    270
                                265
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275
                          280
                                               285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
 290
                       295
                                             300
Arg Leu Ala Arg Gly His Ser Leu
305
                    310
<210> 221
<211> 621
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<sup>&</sup>lt;212> PRT

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<213> Artificial Sequence

<220>

<223> Mutant rep protein: 78 488 GCG

<400> 221 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 3.0 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe

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435
                             440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
   450
                       455
                                              460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                    470
                                         475
Glu His Glu Phe Tyr Val Lys Ala Gly Gly Ala Lys Lys Arg Pro Ala
485 490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
            500
                                 505
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515 520 525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                    550
                                        555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                565
                                    570
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580 585 590
                                585
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
       595
                            600
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
   610
<210> 222
<211> 397
<212> PRT
<213> Artificial Sequence
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<223> Mutant rep protein: rep52 488 GCG

<400> 222 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 10 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 20 25 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 40 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln . 50 55 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 85 90 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 100 105 110 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 120 125 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 130 135 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 150 155 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 165 170 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 180 185 190 180 185 190 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 200 205 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe

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Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 230 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 250 245 Glu His Glu Phe Tyr Val Lys Ala Gly Gly Ala Lys Lys Arg Pro Ala 260 265 270 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 275 .280 285 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 290 295 300 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 310 315 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 325 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 340 345 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 355 360 365 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 370 380 375 380 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 390

<210> 223

<211> 536 <212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep68 488 GCG

<400> 223 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 25 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 40 45 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 70 75 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 150 155 160 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 190 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys

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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
               245
                                     250
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
             260
                                 265
                                                      270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
        275
                            280
                                                 285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                                             300
                        295
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                   310
                                         315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335
                                                          335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
            340
                                 345
                                                     350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365
                             360
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
370 380
                        375
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385 390 395 400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 410 415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                425
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
       435
                           440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                    470
                                        475
Glu His Glu Phe Tyr Val Lys Ala Gly Gly Ala Lys Lys Arg Pro Ala
485 490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
           500
                                505
                                                     510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515
                           520
Arg Leu Ala Arg Gly His Ser Leu
   530
                        535
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<210> 224

<211> 312

<212> PRT

<213> Artificial Sequence

<223> Mutant rep protein: rep40 488 GCG

<400> 224

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 20 25 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 40 45 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55 60 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 90

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Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 100 105 110 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 115 120 125 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 135 130 140 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 150 155 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 165 170 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 185 180 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 195 200 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Thr Thr Phe Glu His Gin 3215 220

Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 230 235 240 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 255 255 Glu His Glu Phe Tyr Val Lys Ala Gly Gly Ala Lys Lys Arg Pro Ala 260 265 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 275 280 285 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 290 295 Arg Leu Ala Arg Gly His Ser Leu 305 310 <210> 225 <211> 621 <212> PRT <213> Artificial Sequence <223> Mutant rep protein: rep78 495 GCC <400> 225 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 25 30 25 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 40 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 50 55 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
85
90
95 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 105 110 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 120 115 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 150 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170

1

Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His

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180
                                 185
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
      195
                             200
                                                 205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
    210
                        215
                                            220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
                     230
                                       . 235
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                    250
                245
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
260 265 270
           260
                                265
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
        275
                            280
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290 295 300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305
                    310
                                         315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                    330
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
370 380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385
                   390
                                         395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405
                                    410
                                                         415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
420 425 430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
       435
                            440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                        455
                                            460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465 470 475 480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
             485
                                    490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
           500
                                505
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515 520 525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 540
                       535
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 545 550 550
                   550
                                        555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
               565
                                  570
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
           580
                               585
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                           600
                                                 605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
    610
                        615
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<sup>&</sup>lt;210> 226

<sup>&</sup>lt;211> 397

<sup>&</sup>lt;212> PRT

<sup>&</sup>lt;213> Artificial Sequence

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<220>
<223> Mutant rep protein: rep52 495 GCC
<400> 226
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
                                    10
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                25
           20
                                                    30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
        35
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
    50
                        55
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                   70
                                        75
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                   90
                                                        95
               85
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
           100
                                105
                                                    110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                            120
                                                125
        115
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
   130
                        135
                                            140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                   150
                                       155
                                                            160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                   170
               165
                                                        175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
            180
                                185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195
                            200
                                                205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
    210
                        215
                                            220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                   230
                                      235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala 260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
       275
                           280
                                                285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
 . 290
                       295
                                           300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 305 310 315 320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                325
                                   330
                                                        335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
           340
                                345
                                                   350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
       355
                           360
                                               365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                       375
                                          380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385
                    390
                                        395
<210> 227
<211> 536
<212> PRT
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<sup>&</sup>lt;213> Artificial Sequence

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<223> Mutant rep protein: rep68 495 GCC

<400> 227 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 1 5 10 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 25 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 40 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 75 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 90 85 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 120 115 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 150 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 245 250 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 -280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 310 315 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 415 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 445 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln

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Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
485
490
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
            500
                                505
                                                     510
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
        515
                             520
 Arg Leu Ala Arg Gly His Ser Leu
 <210> 228
 <211> 312
 <212> PRT
 <213> Artificial Sequence
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Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                25
           20
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
       35
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                        55
                                            60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                    90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100
                               105
                                                   110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
        115
                           120
                                                125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130 135 140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                   150
                                        155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                    170
               165
                                                        175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
           180
                                185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195
                           200
                                                205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
    210
                        215
                                            220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                    230
                                       235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
               245
                                   250
                                                      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
260 265 270
                               265
                                                   270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                           280
                                                285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                        295
   290
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Arg Leu Ala Arg Gly His Ser Leu

310

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<210> 229 <211> 621 <212> PRT <213> Artificial Sequence <220> <223> Mutant rep protein: rep78 497 GCC <400> 229 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 15 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 25 30 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 40 45 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 90 85 95 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 110 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 . 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 150 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 250 245 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 270 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 .310 315 320 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 390 395 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 410

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Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 425 430 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 445 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 495 Ala Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 505 510 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 525 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 535 540 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 555 560 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 565 570 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580
585 585 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 595 600 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 610 615

<210> 230

<211> 397

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep52 497 GCC

<400> 230

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 10 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 20 25 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 40 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 55 60 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 70 75 80 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 85 90 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 100 105 110 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 115 120 125 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 135 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 150 155 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 165 170 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 185 1.90 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser

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```
200
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 215 220
                           215
                                                220
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 235
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245
250
255
                  245
                                       250
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
Ala Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                            280
                                                    285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 290 295 300.
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 305 310 315 320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 345 345
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
355 360 365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
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                                                380
   370
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
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<211> 536
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Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
35 40 45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                          55
                                               60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
85 90 95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
             100
                                   105
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115 120 125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly
    130
                          135
                                               140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145 150 155 160
                                          155
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
165 170 175
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Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His

Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 200

185

190

205

180

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Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
    210
                         215
                                             220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
                    230
                                        235
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
               245
                                    250
                                                        255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
260 265 270
                                265
                                                    270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                            280
                                                285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
    290
                        295
                                            300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                   310
                                       315
                                                            320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
325 330 335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
            340
                                345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                            360
                                               . 365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370
                        375
                                            380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385 390 395 400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
               405
                                   410
                                                        415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                425
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435
                           440
                                                445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
    450
                       455
                                           460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                 470
                                       475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
               485
                                   490
Ala Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
           500
                                505
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Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
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Arg Leu Ala Arg Gly His Ser Leu
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<211> 312

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep40 497 GCC

<400> 232

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 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 20
 25
 30

 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
 35
 40

 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50
 55

 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu

70

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Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 85 90 95 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 100 105 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 115 120 125 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 135 130 140 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 150 155 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 165 170 175 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 180 185 190 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 200 205 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 215 210 220 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 235 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 255 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 260 265 270 Ala Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 275 280 285 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 290 295 300 Arg Leu Ala Arg Gly His Ser Leu 310 <210> 233 <211> 621 <212> PRT <213> Artificial Sequence <223> Mutant rep protein: rep78 497 CGA <400> 233 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 10 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 25 30 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys

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Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 250 245 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys . 260 265 270 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285 Pro Val Glu Asp Ile Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 340 345 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 390 395 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 410 405 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 445 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 Arg Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 510 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 525 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 540 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 545 550 555 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 565 570 575 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580 585 585 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
595 600 605 600 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 610

<210> 234 <211> 397

<212> PRT

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            20
                                  25
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
         35
                             40
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                         55
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                 85
                                      90
                                                          95
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
             100
                                 105
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
        115
                           120
                                                 125
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 130 135 140
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                     150
                                         155
                                                              160
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                 165
                                     170
                                                          175
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
            180
                                185
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195 200 205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
   210
                        215
                                             220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                     230
225
                                         235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
Arg Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
       275
                           280
                                                 285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
   290
                        295
                                             300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305
                    310
                                         315
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                325
                                     330
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
           340
                               345
                                                   350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                        375
                                             380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                    390
<210> 235
<211> 536
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<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep68 497 CGA

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440 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450
460 450 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 475 470 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 Arg Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 505 510 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 Arg Leu Ala Arg Gly His Ser Leu 530 535 <210> 236 <211> 312 <212> PRT <213> Artificial Sequence <220> <223> Mutant rep protein: rep 40 497 CGA Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 35 40 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55 60 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 85 90 . Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 105 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 115 -120 125 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 130 135 140 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 145 150 155 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 170 165 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 185 180 190 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 200 205 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 215 220 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 235 240 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 255 245 250 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 260 265 270 Arg Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 275 280 285

Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp

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<211> 621
<212> PRT
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Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
                                25.
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
        35
                           40
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
                    70
                                       75
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                85
                                    90
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
            100
                               105
                                                   110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
     · 115
                            120
                                                125 ·
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly
                        135
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
                    150
                                       155
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
               165
                                    170
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
                              185
           180
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
       195
                            200
                                               205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
                        215
                                           220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
                   230
                                       235
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                   250
               245
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
           260
                               265
                                                   270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
        275
                            280
                                               285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                       295
                                           300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                   310
                                       315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
              325
                                  330
                                                       335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
           340
                               345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                           360
                                               365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                       375
                                           380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
```

1

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395 390 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 415 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 440 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 Leu Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 525 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 535 540 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 550 555 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 565 570 575 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 585 580 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 595 600 605 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 610 615

<210> 238

<211> 397 <212> PRT

<213> Artificial Sequence

<220>

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Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 185 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 200 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 215 220 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 230 235 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 250 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 265 Leu Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 270 280 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 295 300 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 310 315 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 330 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 345 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 360 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 365 375 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 380 390

<210> 239 <211> 536 <212> PRT

<213> Artificial Sequence

<220>

<400> 239

<223> Mutant rep protein: rep68 497 CTC

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Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly 130 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 145 150 155 160 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His

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180
                                    185
   Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
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                                200
                                                    205
   Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
                          215
                                               220
   Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
                                          235
   Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                        250
  Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                                                            255
                                   265
  Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285
  Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                                               300
  Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                      310
                                          315
  Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                      330
  Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                                                            335
  Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                               360
                                                  365
  Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                          375
                                              380
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385 390 395 400
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                     410
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
420 425 430
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
435 440 445
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450 455 460
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                     470
                                         475
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
495 495
 Leu Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 505
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
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                             520
 Arg Leu Ala Arg Gly His Ser Leu
    530
                         535
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                25
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
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PCT/IB02/04087

Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 85 90 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 105 110 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 115 120 125 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 140 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 150 155 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 165 170 175 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 180 185 190 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 200 205 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 215 220 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 230 235 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 255 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 260 265 Leu Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 275 280 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 290 295 Arg Leu Ala Arg Gly His Ser Leu 305 310

<210> 241

<211> 621

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep78 497 TAC

<400> 241

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 10 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 25 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 40 45 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 75 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 110 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly

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	130	)				139	5				140	)			
Asr 145	. Lys	Val	l Val	l Ası	o Glu 150	ı Cys	Туг	Ile	Pro	Asn 155	Туг	Lev	Lev	Pro	Lys 160
Thr	Glr	1 Pro	Glu	1 Let 165	ı Glr	Tr	Ala	Trp	Th:		Met	Glu	Glr	Tyr 175	Leu
Ser	Ala	суя	180	ı Ası	ı Lev	Thr	Glu	Arg 185	J Lys		Lev	ı Val	Ala 190	Gln	His
Leu	Thr	His	Val		Gln	Thr	Gln 200	Glu		Asn	Lys	Glu 205	Asn	Gln	Asn
Pro	Asr. 210	Ser		Ala	a Pro	Val 215	Ile		Ser	Lys	Thr 220	Ser		Arg	Tyr
Met 225	Glu		ı Val	Gl	7 Trp	Leu		qeA .	Lys	Gly 235	Ile		Ser	Glu	Lys 240
		Ile	Glr	Glu 245	ı Asp		Ala	Ser	Tyr 250	Ile		Phe	Asn	Ala 255	Ala
Ser	Asn	Ser	Arg 260	, Ser	Gln	Ile	Lys	Ala 265	Ala		Asp	Asn	Ala 270	Gly	
Ile	Met	Ser 275	Leu		Lys	Thr	Ala 280	Pro		Tyr	Leu	Val 285	Gly		Gln
Pro	Val 290	Glu		Ile	Ser	Ser 295	Asn		Ile	Tyr	Lys 300	Ile		Glu	Leu
Asn 305	Gly	Tyr	Asp	Pro	Gln 310	Tyr		Ala	Ser	Val 315			Gly	Trp	Ala 320
Thr	Lys	Lys	Phe	Gly 325	Lys	Arg	Asn	Thr	Ile 330	Trp	Leu	Phe	Gly	Pro 335	
Thr	Thr	Gly	Lys 340		Asn	Ile	Ala	Glu 345		Ile	Ala	His	Thr	Val	Pro
Phe	Tyr	Gly 355		Val	Asn	Trp	Thr 360		Glu	Asn	Phe	Pro 365	Phe	Asn	Asp
	370				Val	375					380				
385					Ala 390					395					400
				405					410					415	
			420		Thr			425					430		
		435	-		Gln		440					445			
	450				Leu	455					460				
465					Phe 470					475					480
				485	Val				490					495	
			500		Ile			505				-	510		
		515			Ser		520					525			
	530				Cys	535					540				
545					Cys 550					555					560
				565	Lys				570					575	
			580		Val			585					590		
		595			Gly		600					605	Ala	Cys	Asp
пел	Val 610	Asn	val	Asp	Leu	Asp 615	Asp	Cys	Ile	Phe	Glu 620	Gln			

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 <211> 397
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 <213> Artificial Sequence
 <223> Mutant rep protein: rep52 497 TAC
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 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
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                                 25
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
        35
                             40
                                                 45
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                     70
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                85
                                     90
                                                         95
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100
                                105
                                                    110
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
        115
                           120
                                                 125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130
                         135
Cys Val Asp Lys Met Val Ile: Trp Trp Glu Glu Gly Lys Met Thr Ala
                    150
                                         155
                                                             160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165
                                     170
                                                         175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
            180
                                185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195
                           200
                                                205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
   210
                                             220
                        215
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225
                    230
                                        235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                245
                                    250
                                                         255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
Tyr Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                           280
                                                 285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
    290
                        295
                                            300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305
                   310
                                        315
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                325
                                   330
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
           340
                              345
                                                  350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
355 360 365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
370 380
                        375
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                    390
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<211> 536 <212> PRT <213> Artificial Sequence <223> Mutant rep protein: rep68 497 TAC <400> 243 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 10 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asm Leu Ile 35 40 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 50 55 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 110 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly 130 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 150 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 190 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 230 235 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 270 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 300 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 350 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 390 395 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser

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```
425
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
       435
                            440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
   450
                        455
                                           460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490
Tyr Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
           500
                               505
                                                    510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
       515
                            520
Arg Leu Ala Arg Gly His Ser Leu
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<210> 244

<211> 312

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep40 497 TAC

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Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
    290
                  295
 Arg Leu Ala Arg Gly His Ser Leu
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 <210> 245
 <211> 621
 <212> PRT
 <213> Artificial Sequence
 <223> Mutant rep protein: rep78 498 GCT
 <400> 245
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 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
                                25
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
        35
                           40
                                                45
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                        55
                                            60
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
                    70
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                85
                                    90
                                                        95
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
            100
                                105
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
        115
                            120
                                                125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
                        135
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
                    150
                                        155
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
165 170 175
                165
                                   170
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
            180
                               185
                                                   190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
                            200
                                                205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
   210
                        215
                                           220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225
                    230
                                        235
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245
                                   250
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
           260
                               265
                                                   270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
       275
                           280
                                               285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
    290
                        295
                                            300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305
                   310
                                       315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
               325
                                   330
                                                        335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
           340
                             345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 . 360 365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
```

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375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 390 395 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 415 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 425 420 430 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 Pro Ala Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 505 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 525 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 535 540 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 550 555 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 565 570 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580 585 590 585 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 595 600 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 610

<210> 246

<211> 397

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep52 498 GCT

<400> 246

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Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 165 170 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 180 185 190 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 195 200 205 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 215 220 215 220 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 235 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 250 245 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 260 265 270 Pro Ala Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 275 280 285 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290
295.
300 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 305 310 315 320 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 325 330 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 345 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 355 360 365 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 375 380 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 385 390

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<211> 536 <212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep68 498 GCT

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165
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 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
             180
                                185
                                                      190
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
         195 .
                              200
                                                  205
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
     210
                         215
                                             220
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245 250 255
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                                 265
                                                      270
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                             280
                                                 285
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
    290
                         295
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                   310
                                        315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
325 330 335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
             340
                                 345
                                                     350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355
                             360
                                                  365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370
                         375
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385 390 395 400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405
                                    410
                                                          415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
420 425 430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435
                             440
                                                 445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
   450
                        455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
            470
                                        475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
               485
                                     490
Pro Ala Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
            500
                                505
                                                     510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                            520
       515
Arg Leu Ala Arg Gly His Ser Leu
    530
<210> 248
<211> 312
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep40 498 GCT
<400> 248
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala

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Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 35 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 55 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 70 75 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 85 90 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 100 105 110 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 120 125 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 130 135 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 150 155 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 165 170 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 180 185 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 200 205 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 215 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 230 235 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 260 265 Pro Ala Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 275 280 285 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp . 290 295 300 Arg Leu Ala Arg Gly His Ser Leu 305 <210> 249 <211> 621 <212> PRT <213> Artificial Sequence <223> Mutant rep protein: rep78 499 GCC <400> 249 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 25 30 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 40 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 50 55 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 70 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 95 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 105 110 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu

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Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 270 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 . 345 350 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala Pro Ser Ala Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 540 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 580 585 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 

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 <210> 250
 <211> 397
 <212> PRT
 <213> Artificial Sequence
 <223> Mutant rep protein: rep52 499 GCC
 <400> 250
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
            20
                                 25
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
        35
                                                 45
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
    50
                         55
                                            60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                    70
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                85
                                    90
                                                         95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100
                                105
                                                    110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                            120
                                                125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130
                        135
                                            140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
               165
                                    170
                                                       175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
            180
                                185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                           . 200
        195
                                                205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                                            220
    210
                        215
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                    230
                                       235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                245
                                    250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
            260
                                265
                                                    270
Pro Ser Ala Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
        275
                            280
                                                285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
    290
                        295
                                           300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                    310
                                        315
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                325
                                    330
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
            340
                                345
                                                   350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
       355
                           360
                                              365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                        375
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Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
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Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 445 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 455 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 465 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 Pro Ser Ala Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 510 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 Arg Leu Ala Arg Gly His Ser Leu

<210> 252 <211> 312

<212> PRT

<213> Artificial Sequence

<223> Mutant rep protein: rep40 499 GCC

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260 265 270 Pro Ser Ala Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 275 280 285 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 290 295 300 Arg Leu Ala Arg Gly His Ser Leu 305 <210> 253 <211> 621 <212> PRT <213> Artificial Sequence <223> Mutant rep protein: rep78 503 GCG <400> 253 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 10 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 25 30 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 40 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 75 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 105 110 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 150 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 190 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 230 235 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 270 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro

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Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 375. 370 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 390 395 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 415 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 440 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 455 450 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 495 Pro Ser Asp Ala Asp Ile Ala Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 525 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 535 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 550 555 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 565 570 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 580 585 590 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 595 600 605 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 610 615

<210> 254

<211> 397

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep52 503 GCG

<400> 254

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130
                          135
                                              140
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                   150
                                       155
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165
                                     170
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
             180
                                 185
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
         195
                             200
                                                 205
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                         215
                                             220
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 235 240
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                 245
                                    250
                                                          255
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                                                     270
                                 265
 Pro Ser Asp Ala Asp Ile Ala Glu Pro Lys Arg Val Arg Glu Ser Val
        275
                            280
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
     290
                      295
                                            300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 305 310 315 320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                 325
                                     330
                                                          335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
             340
                                 345
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 355 360 365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
  370
                         375
                                            380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
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<210> 255
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Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
        35
                           40
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                        55
                                            60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65 70 75 80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
               85
                                    90
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
                               105
            100
                                                    110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115 120 125
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Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly

135

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150
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Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
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                                    170
                                                        175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
           180
                               185
                                                   190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
        195
                            200
                                                205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
                        215
                                            220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
                    230
                                       235
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
               245
                                   250
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
           260
                               265
                                                   270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
        275 .
                            280
                                                285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
   290
                        295
                                            300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                   310
                                        315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
           340
                                                    350
                                345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                            360
                                                365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
   370
                        375
                                            380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                   390
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
               405
                                                      415
                                   410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
           420
                                425
                                                   430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435
                            440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
    450
                        455
                                            460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                   470
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
               485
                                    490
                                                       495
Pro Ser Asp Ala Asp Ile Ala Glu Pro Lys Arg Val Arg Glu Ser Val
           500
                               505
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Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
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Arg Leu Ala Arg Gly His Ser Leu
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<210> 256
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<223> Mutant rep protein: rep40 503 GCG
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Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys

<400> 256

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys

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Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
35 40
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                         55
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                85
                                     90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100
                                 105
                                                      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
        115
                             120
                                                  125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                         135
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                    150
                                        155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165
                                     170
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180 185 190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195
                             200
                                                 205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 215 220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225 230 235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                245
                                     250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
            260
                                                     270
                                 265
Pro Ser Asp Ala Asp Ile Ala Glu Pro Lys Arg Val Arg Glu Ser Val
        275
                            280
                                                 285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                       295
                                             300
Arg Leu Ala Arg Gly His Ser Leu
305
                    310
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<210> 257

<211> 621

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep78 510 GCA

<400> 257

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Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 145 150 155 160 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ala Val Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 545 550 560 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr

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585 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 595 600 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 610 615 <210> 258 <211> 397 <212> PRT <213> Artificial Sequence <220> <223> Mutant rep protein: rep52 510 GCA <400> 258 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 20 25 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 45 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 90 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 100 105 110 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 115 120 125 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 130 135 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 150 155 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 170 175 165 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val I80 185 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 195 200 205 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 215 220 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 235 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 255 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 260 265 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ala Val 275 285 280 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 290 295 300 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 305 310 315 320 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 325 . 330 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 340 350 345 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr

360

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Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 370 375 380

Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 395 390 395

<210> 259

<211> 536

<212> PRT <213> Artificial Sequence

<220>

<223> Mutant rep protein: rep68 510 GCA

<400> 259 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr-Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala

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370 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 390 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 425 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 440 435 445 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 465 470 480 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ala Val 500 505 510 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 Arg Leu Ala Arg Gly His Ser Leu <210> 260 <211> 312 <212> PRT <213> Artificial Sequence <223> Mutant rep protein: rep40 510 GCA <400> 260 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 10 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 20 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 35 40 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 85 90 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 100 105 110 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 115 120 125 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 135 140 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 150 155 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 165 170 175 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 180 185 190 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 195 200 205 200 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 215 220

Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln

230

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Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ala Val Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp Arg Leu Ala Arg Gly His Ser Leu 

<210> 261

<211> 621

<212> PRT '

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep78 511 GCA

<400> 261

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala

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325
                                      330
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                                  345
             340
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 . 360 365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405
                                      410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435
                             440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455 460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                 470
                                          475
                                                                480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ala Val
                                  505
            500
                                                       510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515 520 525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                    550
                                          555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
565 570 575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580 585 590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
       595
                            600
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
 610
                         615
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<210> 262 <211> 397

<212> PRT <213> Artificial Sequence

<220>

<223> Mutant rep protein: rep52 511 GCA

<400> 262 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 20 30 25 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 35 40 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55 60 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 85 95 90 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 105

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Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ala Val Ala Gin Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln <210> 263

<211> 536 <212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep68 511 GCA

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu . -310-

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120
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly
    130
                         135
                                             140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145
                    150
                                         155
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
                165
                                    170
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
180 185 190
           180
                               185
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
       195
                            200
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
                    230
                                       235
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245 255
                245
                                    250
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
          260
                                265
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
        275
                            280
                                                 285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                        295
    290
                                            300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305 310 315
                                        315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325
                                    330
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345
                               345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370
                        375
                                            380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                  390
                                        395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
               405
                                                        415
                                    410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
   450
                        455
                                           460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                        475
                   470
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
               485
                                                        495
                                    490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ala Val
           500
                                                    510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
       515
                           520
Arg Leu Ala Arg Gly His Ser Leu
                        535
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<sup>&</sup>lt;210> 264

<sup>&</sup>lt;211> 312

<sup>&</sup>lt;212> PRT

<sup>&</sup>lt;213> Artificial Sequence

<sup>&</sup>lt;220>

<sup>&</sup>lt;223> Mutant rep protein: rep40 511 GCA

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<400> 264
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
                                    10
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                25
                                                    30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                           40
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                       55
                                          60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                   70
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
               85
                                    90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100
                                105
                                                   110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
        115
                           120
                                               125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
   130
                       135
                                          140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                   150
                                       155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
               165
                                    170
                                                       175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
           180
                               185
                                                   190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                           200
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                   230
                                       235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
               245
                                   250
                                                       255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
           260
                                                   270
                               265
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ala Val
       275
                         280
                                               285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
 290
                      295
                                           300
Arg Leu Ala Arg Gly His Ser Leu
                   310
<210> 265
<211> 621
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<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep78 512 GCT

<400> 265

Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 145 150 155 160 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn . 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240 Gin Trp Ile Gin Glu Asp Gin Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Ala Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 540 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu

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565 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 580 585 590 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 595 600 605 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 610 615 <210> 266 <211> 397 <212> PRT <213> Artificial Sequence <223> Mutant rep protein: rep52 512 GCT <400> 266 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 3.0 15 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 20 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 35 40 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 85 90 95 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 100 105 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 115 120 125 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 130 135 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 150 155 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 165 170 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 180 185 190 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 195 200 205 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 215 220 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 230 235 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 260 265 270 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Ala 280 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 290 295 300 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 305 310 315 320 315 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 325 330 335 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu

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<210> 267 <211> 536 <212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep68 512 GCT

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1 10 15 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 25 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 45 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 70 75 · Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 190 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 230 235 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 270 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 280 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 345 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp

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360 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 375 380 Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 390 395 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 495 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Ala
500 505 510 505 510 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 Arg Leu Ala Arg Gly His Ser Leu

<210> 268

<211> 312 <212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep40 512 GCT

<400> 268

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 20 25 30 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 35 -40 45 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 100 105 110 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 120 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 135 140 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 150 155 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 165 170 175 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 180 185 190 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 195 200 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe

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Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Ala Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp Arg Leu Ala Arg Gly His Ser Leu 

<210> 269 <211> 621

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep78 516 GCG

<400> 269 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala

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305
                     310
                                         315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
               325
                                     330
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                                                     350
           . 340
                                 345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                             360
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                        375
                                             380
    370
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                   390
                                        395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                 425
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435
                             440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
   450
                        455
                                            460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                   470
                                        475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
            500
                                505
Ala Gln Pro Ala Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
        515
                          520
                                                 525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                        535
                                             540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                   550
                                       555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
565 570 575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580 585 590
                                585
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
595 600 605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                        615
<210> 270
<211> 397
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep52 516 GCG
<400> 270
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
            20
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                                                 45
       35
                            40
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                        55
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                   70
                                        75
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
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Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100
                                105
                                                    110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
        115
                            120
                                                125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130
                        135
                                            140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                    150
                                        155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
               165
                                    170
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
            180
                                185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195
                                                205
                           200
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 220
                       215
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                    230
                                      235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                   250
               245
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                               265
                                                   270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
        275
                           280
                                               285
Ala Gln Pro Ala Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                       295
                                           300
   290
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                   310
                                       315
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                                                       335
               325
                                   330
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
           340
                                345
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
       355
                           360
                                               365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
 370
                        375
                                           380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385
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<210> 271

<211> 536

<212> PRT <213> Artificial Sequence

<220>

<223> Mutant rep protein: rep68 516 GCG

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105
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
      115
                            120
                                                125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly
                        135
                                            140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145 150 155 160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
165 170 175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
                                185
            180
                                                     190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
       195
                           200
                                                205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
                        215
   210
                                            220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245 250 255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
260 265 270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
       275
                          280
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                        295
                                             300
  290
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                    310
                                         315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                    330
                325
                                                         335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
            340
                                345
                                                    350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
   370
                        375
                                            380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
               405
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
           420
                               425
                                                    430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
435
440
445
       435
                           440
                                                445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
   450
                        455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                   470
                                        475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                                                         495
                485
                                    490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
           500
                              505
                                                    510
Ala Gln Pro Ala Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515 520 525
Arg Leu Ala Arg Gly His Ser Leu
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<210> 272

<211> 312

<212> PRT

<213> Artificial Sequence

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<223> Mutant rep protein: rep40 516 GCG
<400> 272
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                                    30
                                25
            20
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
       35
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                                            60
                        55
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                                       75
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                   90
                85
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100
                                105
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
       115
                            120
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                                            140
   130
                        135
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                                       155
                                                            160
                    150
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                   170
               165
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                                    190
            180
                                185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
       195
                            200
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                                            220
                        215
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                                     235
                                                            240
                    230
225
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                                                    270
            260
                                265
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                                285
                           280
       275
Ala Gln Pro Ala Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                        295
                                            300
 290
Arg Leu Ala Arg Gly His Ser Leu
305
                    310
<210> 273
<211> 621
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep78 517 GCT
<400> 273
Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
            20
                                25
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
                                                45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
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55 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 70 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 90 85 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 145 150 160 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 185 180 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
210 215 215 220 210 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 265 260 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 295 290 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 415 410 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 430 420 425 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 460 450 455 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 475 470 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 495 485 490 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 505 510 Ala Gln Pro Ser Ala Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 525 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 540

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Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 

<210> 274 <211> 397 <212> PRT

<213> Artificial Sequence

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<223> Mutant rep protein: rep52 517 GCT

<400> 274 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55 60 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val Ala Gln Pro Ser Ala Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys

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335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                                                    350
                               345
            340
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
                             360
                                                 365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                                             380
                         375
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                     390
<210> 275
<211> 536
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep68 517 GCT
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Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
20 25 30
                                 25
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
                             40
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                                             60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 75 70 80
                                         75
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
85 90 95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
100 105 110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
                             120
        115
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly
                         135
                                             140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145 150 155 160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
165 170 175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
            180
                                 185
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
195 200 205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
                        215
                                             220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225 230 240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245
                                     250
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                                 265
            260
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
        275
                            280
                                                 285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                        295
    290
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                    310
                                         315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
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Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 365 360 355 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400 390 385 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 425 420 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 445 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 455 460 450 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 475 470 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 490 485 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 505 500 Ala Gln Pro Ser Ala Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 Arg Leu Ala Arg Gly His Ser Leu 530 535

<210> 276

<211> 312

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep40 517 GCT

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 10 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 20 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 40 35 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 55 60 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 70 75 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 95 90 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 100 105 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 120 125 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 130 135 140 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 155 150 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 165 170 175 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 185 190 180 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser

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200
                                                  205
         195
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
    210
                        215
                                             220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                     230
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                   250
                                                       255
                245
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
            260
                                265
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
275 280 285
Ala Gln Pro Ser Ala Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
   290 ·
                         295
Arg Leu Ala Arg Gly His Ser Leu
305
                    310
<210> 277
<211> 621
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep78 517 AAC
<400> 277
Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
            20
                                 25
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
       35
                            40
                                                45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                        55
                                            60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                85
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
            1-00
                                105
                                                     110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
                            120
                                                125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
                    150
                                         155
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
                165
                                     170
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
            180
                                                     190
                                185
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
       195
                           200
                                                205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 220
                      215
                                           220
    210
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 240
Gin Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245 250 255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                                                    270
            260
                                265
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Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln

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Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
   290
                        295
                                            300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                    310
                                        315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325
                                    330
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                                                    350
            340
                               345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                            360 ·
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
   370
                        375
                                           380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                   390
385
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
               405
                                    410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
           420
                               425
                                                    430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                           440
       435
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
   450
                       455
                                           460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                   470
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                                                        495
                                   490
               485
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                               505
                                                   510
           500
Ala Gln Pro Ser Asn Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515 520 525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                       535
                                            540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                   550
                                        555
545
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                                                        575
                                   570
                565
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
                                                    590
                               585
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                           600
                                                605
       595
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
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<210> 278 <211> 397

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep52 517 AAC

<400> 278

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Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
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                                105
                                                    110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115
                           120
                                               125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                        135
                                           140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                    150
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
              165
                                    170
                                                        175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
           180
                                185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195
                           200
                                               205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
    210
                        215
                                           220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225 230 235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                                        255
                245
                                    250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                               265
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                             285
                           280
        275
Ala Gln Pro Ser Asn Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
   290
                       295
                                            300.
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305
                    310
                                        315
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                325
                                                        335
                                    330
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
           340
                              345
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
        355
                                              365
                            360
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                        375
                                            380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385
<210> 279
<211> 536
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep68 517 AAC
<400> 279
Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
                                    10
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
20 25 30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
       35
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
   50
                       55
                                           60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
                    70
```

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Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val Ala Gln Pro Ser Asn Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp Arg Leu Ala Arg Gly His Ser Leu 

<210> 280 <211> 312

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<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep40 517 AAC
<400> 280
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
            20
                                25
                                                    30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                           40
       35
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
   50
                        55
                                            60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                85
                                    90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                                    110
            100
                                105
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
        115
                           120
                                               125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                                           140
                        135
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                    150
145
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                                        175
                165
                                    170
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
           180
                               185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 195 200 205
        195
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                                            220
   210
                        215
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                    250
                245
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                                                    270
           260
                               265
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                               285
        275
                           280
Ala Gln Pro Ser Asn Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                        295
                                            300
Arg Leu Ala Arg Gly His Ser Leu
305
                    310
<210> 281
<211> 621
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep78 518 GCA
<400> 281
Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
                                                       .15
                                    10
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
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Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 235 230 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Eys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 . 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 495 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val Ala Gln Pro Ser Thr Ala Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp

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```
520
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
    530
                       535
                                           540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                    550
                                       555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                565
                                   570
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
                              585
           580
                                                   590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                                               605
                           600
       595
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
    610
<210> 282
<212> PRT
<213> Artificial Sequence
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<211> 397

<223> Mutant rep protein: rep52 518 GCA

<400> 282 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 10 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 20 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 40 35 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 55 60 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 70 75 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 85 90 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 105 110 100 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 115 120 125 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 135 130 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 150 155 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 175 165 170 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 180 185 190 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 205 195 200 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 215 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 235 240 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 260 265 270 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 285 280 Ala Gln Pro Ser Thr Ala Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp

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Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 310 315 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 330 325 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 350 345 340 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 355 360 365 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 380 375 370 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 390 <210> 283 <211> 536 <212> PRT <213> Artificial Sequence <223> Mutant rep protein: rep68 518 GCA <400> 283 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 25 30 25 20 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 45 35 40 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 60 50 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 125 115 120 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 135 140 150 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 175 170 165 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 . 185 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 220 210 215 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 230 235 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 270 260 265 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu

295

Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala

300

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```
310
                                        315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
               325
                                 - 330
                                                        335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
           340
                               345
                                                    350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                           360
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                   390
                                       395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
               405
                                   410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                                   430
           420
                               425
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                          440
       435
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
   450
                       455
                                           460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                  470
465
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                                   490
                                                       495
               485
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
           500
                               505
                                                   510
Ala Gln Pro Ser Thr Ala Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515
                           520
Arg Leu Ala Arg Gly His Ser Leu
   530
                        535
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<210> 284

<211> 312

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep40 518 GCA

<400> 284 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 1 15 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 25 20 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 40 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 60 55 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 70 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 85 90 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 100 105 110 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 115 120 125 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 135 140 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 150 145 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg

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Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val Ala Gln Pro Ser Thr Ala Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp Arg Leu Ala Arg Gly His Ser Leu 

<210> 285

<211> 621 <212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep78 519 GCG

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1 10 15 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys

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```
260
                                                        270
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
         275
                              280
                                                  285
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
 305
                     310
                                         315
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325
                                     330
                                                           335
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
             340
                                  345
                                                       350
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
         355
                              360
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                         375
                                              380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385 390 395 400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 410 415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                                      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
435
440
                             440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465 470 475 480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
500 505
                                 505
                                                      510
Ala Gln Pro Ser Thr Ser Ala Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                            520
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                        535
                                             540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                    550
                                         555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
565 570
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580 585 590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
       595
                           600
                                                 605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                        615
<210> 286
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<211> 397 <212> PRT

<213> Artificial Sequence

<223> Mutant rep protein: rep52 519 GCG

<400> 286

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 20 25 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys

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Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                          55
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                     70
                                          75
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
85 90 95
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
             100
                                  105
                                                      110
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                             120
                                                  125
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
     130
                         135
                                             140
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                    150
                                         155
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                 185
                                                      190
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
         195
                             200
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                        215
                                             220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 235 240
                                         235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                                 265
                                                     270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
        275
                            280
                                                 285
Ala Gln Pro Ser Thr Ser Ala Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                       295
                                             300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 305 310 315 320
                                         315
                                                              320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 325
                                                          335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
           340
                                345
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
355 360 365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 370 380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                    390
```

<sup>&</sup>lt;210> 287

<sup>&</sup>lt;211> 536

<sup>&</sup>lt;212> PRT

<sup>&</sup>lt;213> Artificial Sequence

<sup>:220&</sup>gt;

<sup>&</sup>lt;223> Mutant rep protein: rep68 519 GCG

<sup>&</sup>lt;400> 287

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 1 5 10 15 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 25 30 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 40 45 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu

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Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 - 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
435 440 445 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val Ala Gln Pro Ser Thr Ser Ala Ala Glu Ala Ser Ile Asn Tyr Ala Asp Arg Leu Ala Arg Gly His Ser Leu 

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<210> 288
  <211> 312
  <212> PRT
  <213> Artificial Sequence
  <220>
 <223> Mutant rep protein: rep40 519 GCG
 <400> 288
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
                                       10
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
             20
                                                       30
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
         35
                              40
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55 60
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65 70 75 80
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                      90
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
             100
                                  105
                                                      110
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                              120
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
     130
                         135
                                             140
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                     150
                                         155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165 170 175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                  185
                                                      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
         195
                             200
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                        215
                                             220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 235 240
                                        235
                                                               240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                             280
                                                 285
Ala Gln Pro Ser Thr Ser Ala Ala Glu Ala Ser Ile Asn Tyr Ala Asp
  290
                       295
                                              300
Arg Leu Ala Arg Gly His Ser Leu
                    310
<210> 289
<211> 621
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep78 598 GCA
Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
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Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 ' Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val

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Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                                                525
        515
                            520
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
530 540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 545 550 560
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 565 570 575
                565
                                570
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580 585 590
           580
Ile His His Ile Met Ala Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
       595
                            600
                                                 605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
<210> 290
<211> 397
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep52 598 GCA
<400> 290
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
           20
                                25
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                            40
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                    90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                                     110
           IOO
                                105
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                            120
                                                 125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130 135 140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                                       , 155
                    150
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                    170
               165
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180 185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195
                            200
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                                             220
                         215
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                    230
                                        235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245 250 255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                                265
                                                    270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
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Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr Ile His His Ile Met Ala Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 370 375 380 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 

<210> 291

<211> 621

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep78 598 GAC

<400> 291 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu

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```
290
                                             300
                        295
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                   310
                                      315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
               325
                                    330
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
            340
                                345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355
                            360
                                                365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                       375
                                           380
    370
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385 390 395 400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
               405
                                    410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430
                                425
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
       435 .
                           440
                                                445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
  450
                       455
                                           460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                 470
                                       475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
            500
                                505
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
       515
                           520
                                             - 525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
530 540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                   550
                                        555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                565
                                   570
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580 585 590
           580
                               585
Ile His His Ile Met Asp Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
      595 -
                          600
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                        615
   610
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<210> 292

<211> 397

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep52 598 GAC

400> 292

 Met Glu Leu Val Gly Trp
 Leu Val Asp Lys
 Lys
 Gly Ile Thr Ser Glu Lys
 15

 Gln Trp
 Ile Gln Glu Asp Zo
 Gln Ala Ser Tyr
 Ile Ser Phe Asn Ala Ala Ala Ala Zo
 30

 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
 35
 40
 45

 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50
 55
 60

 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65
 70
 75
 11

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Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                     90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100
                                105
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                           120
                                                125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130
                        135
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                                       155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165
                                    170
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
           180
                               185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 195 200 205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
    210
                        215
                                            220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                    230
                                        235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                245
                                   250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
       275
                           280
                                                285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 290 295 300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                    310
                                       315
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                325
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
           340
                              345
                                                  350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
      355
                            360
                                                365
Ile His His Ile Met Asp Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 370 380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385
                    390
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<210> 293

<211> 621 <212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep78 598 AGC

 <400> 293

 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 1
 5
 10
 15

 Glu His Leu Pro Gly Ile Ser Asp Ser Asp Leu Asp Trp Val Ala Glu 20
 25
 30

 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35
 40
 45

 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 50
 50

 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65
 70
 75

 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu

# -344-

				0-					00					n E	
Thr	Thr	Gl v	17a 1	85 Tage	Ser	Met	Va1	T.e.11	90 G1v	Arg	Dhe	ī.eu	Ser	95 Gln	Tle
1111	1111	CTY	100	Lys	501	1100	var	105	GLY	AL 9	2 110	ДСЦ	110	0111	
Arg	Glu	Lys 115		Ile	Gln	Arg	Ile 120	Tyr	Arg	Gly	Ile	Glu 125	Pro	Thr	Leu
Pro	Asn 130	Trp	Phe	Ala	Val	Thr 135			Arg	Asn	Gly 140		Gly	Gly	Gly
Asn 145		Val	Val	Asp	Glu 150		Tyr	Ile	Pro	Asn 155		Leu	Leu	Pro	Lys 160
	Gln	Pro	Glu	Leu 165		Trp	Ala	Trp	Thr 170	Asn	Met	Glu	Gln	Tyr 175	
Ser	Ala	Cys	Leu 180	Asn	Leu	Thr	Glu	Arg 185		Arg	Leu	Val	Ala 190	Gln	His
Leu	Thr	His 195	Val	Ser	Gln	Thr	Gln 200	Glu	Gln	Asn	Lys	Glu 205	Asn	Gln	Asn
	210					215				Lys	220				
225					230					Gly 235					240
				245					250	Ile				255	
			260				_	265		Leu			270		
		275					280			Tyr		285			
	290					295				Tyr	300		_		_
305					310					Val 315					320
				325					330	Trp				335	
			340					345		Ile			350		
		355					360			Asn		365			
	370					375				Glu	380				
385			-		390					Gly 395					400
				405					410	Ile				415	
			420					425		Val			430		
		435					440			Asp		445			
	450					455				Gly	460				
465					470					Asp 475					480
		•		485				_	490	Ala				495	
			500					505		Arg			510	_	
		515					520			Ser		525			
_	530			-	-	535	_			Gly	540				
9ne 545	PTO	cys	wr.d	GTU	550	GIU	Arg	Met	ASD	Gln 555	ASII	ser	VSII	116	560
Phe	Thr	His	Gly	Gln 565	ГÀЗ	Asp	Cys	Leu	Glu 570	Cys	Phe	Pro	Val	Ser 575	Glu

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Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr Ile His His Ile Met Ser Lys Val Pro Asp Ala Cys Thr Ala Cys Asp Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 

<210> 294 <211> 397 <212> PRT

<213> Artificial Sequence

<223> Mutant rep protein: rep52 598 AGC

<400> 294 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 130 135 140 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr

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```
355
                               360
  Ile His His Ile Met Ser Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
    370
                        375
                                               380
  Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
  385
                      390
 <210> 295
 <211> 621
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Mutant rep protein: rep78 600 GCG
 <400> 295
 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
                                  25
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
         35
                              40
                                                   45
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                          55
                                              60
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                 85
                                    90
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
100 105 110
                                 105
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115
120
125
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly
     130
                          135
                                              140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145 150 155 160
                                         155
                                                               160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
                 165
                                     170
                                                          175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
            180
                                 185 ·
                                                       190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
195 200 205
                              200
                                                  205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
                         215
                                             220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225 230 235 240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245 250 255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
            260
                                 265
                                                      270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
275 280 285
                             280
                                                 285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                         295
                                             300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305
                    310
                                         315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325
                                     330
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
            340
                                345
                                                      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355
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Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 375 370 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 390 395 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 415 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 445 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 495 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 505 500 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 525 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 535 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 550 545 555 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 565 570 575 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 580 585 Ile His His Ile Met Gly Lys Ala Pro Asp Ala Cys Thr Ala Cys Asp 600 595 605 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 615

<210> 296

<211> 397

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep52 600 GCG

<400> 296

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 10 15 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 35 40 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 55 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 75 70 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 85 90 95 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 100 105 110 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 115 120 125 120 125 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 140 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala

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Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 255 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 260 265 270 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 325 330 335 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr Ile His His Ile Met Gly Lys Ala Pro Asp Ala Cys Thr Ala Cys Asp Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln <210> 297 <211> 621 <212> PRT <213> Artificial Sequence <220> <223> Mutant -rep protein: rep78 600 CCG <400> 297 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 25 30 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 

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Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln . 275 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450
455
460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 525 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 580 585 Ile His His Ile Met Gly Lys Pro Pro Asp Ala Cys Thr Ala Cys Asp Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 

<210> 298 <211> 397

-350-

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<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep52 600 CCG
<400> 298
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
                                      10
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                 25
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                            40
        35
                                                 45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                85
                                     90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                105
            100
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115 120 125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130 135 140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                                       . 155
                                                              160
145
                     150
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165
                                    170
                                                         175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180 185 190
                                185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 195 200 205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                        215
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                    230
                                         235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                245
                                    250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
        275
                                                  285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
    290
                        295
                                             300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                    310
                                         315
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 325 330 335
                325
                                   330
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                                                  350
           340
                               345
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
355 . 360 365
Ile His His Ile Met Gly Lys Pro Pro Asp Ala Cys Thr Ala Cys Asp
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 370
                                             380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
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<sup>&</sup>lt;211> 621

<sup>&</sup>lt;212> PRT

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<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep78 601 GCA

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435
                               440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                                                460
    450
                         455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                      470
                                           475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
500 505 510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515 520 525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
530 540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 545 550 560
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
565 570 575
                 565
                                      570
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580 585 590
            580
Ile His His Ile Met Gly Lys Val Ala Asp Ala Cys Thr Ala Cys Asp
      595
                             600
                                                    605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                         615
  610
<210> 300
<211> 397
<212> PRT
<213> Artificial Sequence
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<223> Mutant rep protein: rep52 601 GCA

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20 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys -35 -40 45 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80 65 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 85 90 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 105 100 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 115 120 125 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 130 135 140 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 145 150 155 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 165 170 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 180 185 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 195 200 205 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 215

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Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 235 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 255 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 260 265 270 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 275 280 285 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 290 295 300 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 30Š 310 315 320 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 335 325 330 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 345 340 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 355 360 365 Ile His His Ile Met Gly Lys Val Ala Asp Ala Cys Thr Ala Cys Asp 375 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 390

<210> 301

<211> 621

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep 78 335 420 495 GCT GCC GCC

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225
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
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                                   250
           · 245
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                               265
           260
                                                   270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                                             285
        275
                           280
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                                           300
                        295
   290
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                   310
                                        315
                                                            320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Ala Ala
              325
                                   330
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                               345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355
                            360
                                               365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
   370
                       375
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                   390
                                        395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                   410
                                                        415
               405
Ile Val Thr Ala Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                              425
                                                   430
            420
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450 455 460
                       455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                   470
                                       475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
              485
                                    490
                                                        495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                               505
           500
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                           520
                                               525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                                            540
   530
                       535
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                   550
                                       555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
565 570 575
                                  570
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580 585
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
       595
                           600
                                               605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                        615
<210> 302
<211> 397 <212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep52 335 420 495 GCT GCC GCC
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Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
             20
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
        35
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
    50
                         55
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                 85
                                     90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Ala Ala
100 105 110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
        115
                             120
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                         135
                                              140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                     150
                                         155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                     170
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180 185 190
            180
                                185
Ile Val Thr Ala Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195
                            200
                                                 205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 215 220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225
                     230
                                        235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                 245
                                    250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
        275
                             280
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                         295
                                             300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305
                    310
                                         315
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                                   330
                                                          335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 340 345
          340
                               345
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
355 360 365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                        375
                                             380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385
                    390
<210> 303
<211> 536
<212> PRT
<213> Artificial Sequence
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<sup>&</sup>lt;223> Mutant rep protein: rep68 335 420 495 GCT GCC GCC

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu

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			20					25					30		
Lys	Glu	Trp 35	Glu	Leu	Pro	Pro	Asp 40	Ser	Asp	Met	Asp	Leu 45	Asn	Leu	Ile
Glu	Gln 50	Ala	Pro	Leu	Thr	Val 55	Ala	Glu	Lys	Leu	Gln 60	Arg	Asp	Phe	Leu
Thr 65	Glu	Trp	Arg	Arg	Val 70	Ser	Lys	Ala	Pro	Glu 75	Ala	Leu	Phe	Phe	Val 80
Gln	Phe	Glu	Lys	Gly 85	Glu	Ser	Tyr	Phe	His 90	Met	His	Val	Leu	Val 95	Glu
Thr	Thr	Gly	Val 100	Lys	Ser	Met	Val	Leu 105	Gly	Arg	Phe	Leu	Ser 110	Gln	Ile
_		115				_	120	_		_		Glu 125			
Pro	Asn 130	Trp	Phe	Ala	Val	Thr 135	Lys	Thr	Arg	Asn	Gly 140	Ala	Gly	Gly	Gly
Asn 145	Lys	Val	Val	Asp	Glu 150	Cys	Tyr	Ile	Pro	Asn 155	Tyr	Leu	Leu	Pro	Lys <sup>.</sup>
Thr	Gln	Pro	Glu	Leu 165	Gln	Trp	Ala	Trp	Thr 170	Asn	Met	Glu	Gln	Tyr 175	Leu
		_	180		_		_	185	_	_		Val	190		_
		195					200				_	Glu 205			
	210					215		_		_	220	Ser			_
225					230			•		235		Thr		_	240
				245	_				250			Phe		255	
			260				-	265			_	Asn	270	_	_
		275					280					Val 285		_	
	290					295		_		_	300	Ile			_
305	-	_	•		310	_				315		Leu			320
_			•	325					330			Phe		335	
		_	340	_	•			345				His	350		
		355	-			_	360					9ro 365			
	370					375		_			380	Lys		_	
385					390					395		Ser			400
	-			405	_				410		_	Pro		415	
			420					425				Asp	430		
		435					440			_	_	Met 445			
	450					455					460	Val			
465					470					475		Val			480
				485		-		_	490	•	_	Lys		495	
PTO	ser	Asp	500	Asp	тте	ser	GIU	505	туѕ	Arg	val	Arg	510	96T	· val

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Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
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                             520
 Arg Leu Ala Arg Gly His Ser Leu
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 <210> 304
 <211> 312
 <212> PRT
 <213> Artificial Sequence
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 <400> 304
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
            20
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
        35
                             40
                                                 45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
    50
                        55
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                85
                                     90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Ala Ala
            100
                                 105
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
        115
                             120
                                                 125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130
                        135
                                             140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                   150
                                        155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165
                                     170
                                                         175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180 190
                                185
                                                     190
Ile Val Thr Ala Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195
                            200
                                                205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
   210
                        215
                                            220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 235 240
                                       235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                245
                                    250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
                                265
                                                     270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
        275
                           280
                                                285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
   290
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                                            300
Arg Leu Ala Arg Gly His Ser Leu
305
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<210> 305
<211> 621
<212> PRT
<213> Artificial Sequence
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<223> Mutant rep protein: rep78 39 140 GCA GCC

<400> 305 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 25 Lys Glu Trp Glu Leu Pro Ala Asp Ser Asp Met Asp Leu Asn Leu Ile 35 40 45 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 120 125 115 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Ala Ala Gly Gly Gly 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 145 150 155 160 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 190 180 185 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 215 220 210 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 -280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 380 370 375 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 415 410 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 445 435 440 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln

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Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 495 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 510 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 520 525 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 540 540 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 550 555 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 565 570 575 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 580 . 585 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 595 600 605 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 610 615

<210> 306

<211> 536

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep68 39 140 GCA GCC

<400> 306

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 25 30 Lys Glu Trp Glu Leu Pro Ala Asp Ser Asp Met Asp Leu Asn Leu Ile 40 45 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 50 55 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Ala Ala Gly Gly 130 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 150 155 160 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 190 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 230 235 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala

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245
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                                                          255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
            260
                                265
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                           280
        275
                                                285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
    290
                         295
                                             300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305
                    310
                                        315
                                                              320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335
                                   330
                                                         335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
340 345 350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355
                             360
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                        375
                                             380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                   390
385
                                        395
                                                              400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
               405
                                  410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430
                               425
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                            440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
    450
                        455
                                            460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                   470
                                        475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
           500
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Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
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Arg Leu Ala Arg Gly His Ser Leu
<210> 307
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<211> 621

<212> PRT

<213> Artificial Sequence

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<223> Mutant rep protein: rep78 279 428 451 GCC GCT GCC

<400> 307

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 10 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 25 30 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 40 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 50 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75... 80 75 ---Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105

Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 120 115 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 150 155 160 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 190 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 270 Ile Met Ser Leu Thr Lys Ala Ala Pro Asp Tyr Leu Val Gly Gln Gln
275
280
285 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 415 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ala Asp Gly Asn Ser 420 425 425 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 440 Glu Leu Ala Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 495 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 510 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 520 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 535 540 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 545 550 555 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 565 570 575 570 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 585 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp

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595 600 605 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 610 615 620

<210> 308

<211> 397 <212> PRT

<213> Artificial Sequence

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<223> Mutant rep protein: rep52 279 428 451 GCC GCT GCC

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375
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385
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<210> 309
<211> 536
<212> PRT
<213> Artificial Sequence
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                                25
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
        35
                           40
                                                45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                       55
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
                   70
                                       75
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
               85
                                   90
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
            100
                                105
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
                           120
       115
                                               125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly
                        135
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145 150 155 160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
               165
                                   170
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
           180
                               185
                                                   190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
       195
                           200
                                                205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
                      215
                                           220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
                   230
                                      235
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                   250
               245
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
           260
                               265
                                                   270
Ile Met Ser Leu Thr Lys Ala Ala Pro Asp Tyr Leu Val Gly Gln Gln
       275
                           280
                                              285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                       295
                                           300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                   310
                                        315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
               325
                                                       335
                                   330
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
           340
                              345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                           360
                                               365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
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Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ala Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Ala Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp Arg Leu Ala Arg Gly His Ser Leu

<210> 310

<211> 312

<212> PRT

<400> 310

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep40 279 428 451 GCC GCT GCC

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Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe

Glu Leu Ala Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln

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Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                245
                                    250
Glu His Glu Phe Tyr Val Lys Lys Gly Ala Lys Lys Arg Pro Ala
           260
                               265
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
       275
                           280
                                               285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
   290
                       295
                                           300
Arg Leu Ala Arg Gly His Ser Leu
<210> 311
<211> 621
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep78 125 237 600 GCG GCC GCG
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Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Ala Pro Thr Leu Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 145 150 155 160 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Ala Ser Glu Lys 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala

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Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
              340
                                  345
                                                       350
  Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
          355
                              360
                                                  365
  Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
     370
                        375
                                             380
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385 390 395 400
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 410 415
                                     410
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                 425
                                                      430
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
         435
                             440
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
    450
                         455
 Glu Vai Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                    470
                                         475
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                505
                                                     510
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
        515
                            520
                                                  525
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 540
                        535
                                              540
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys. 545 550 555
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu.
                                    570
                                                         575
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580
585
 Ile His His Ile Met Gly Lys Ala Pro Asp Ala Cys Thr Ala Cys Asp
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                            600
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
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 <211> 397
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 <213> Artificial Sequence
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
           20
                                                   30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                            40
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                       55
                                            60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65 70 75 80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
               85
                                    90
                                                        95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
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Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
       115
                          120
                                               125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130
                        135
                                            140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                    150
                                       155
                                                             160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
               165
                                    170
                                                        175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
           180
                               185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
       195
                                                205
                            200
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
    210
                        215
                                            220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                    230
225
                                        235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                245
                                   250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
        275
                            280
                                                285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                        295
    290
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305
                    310
                                       315
                                                            320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
               325
                                    330
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
           340
                               345
                                                   350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
                            360
                                               365
Ile His His Ile Met Gly Lys Ala Pro Asp Ala Cys Thr Ala Cys Asp 370 380
                       375
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                    390
<210> 313
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<210> 313 <211> 536 <212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep68 125 237 600 GCG GCC GCG

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120
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly
                         135
                                            140
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145 150 155 160
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
                 165
                                      170
                                                           175
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
         195
                             200
                                                 205
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
     210
                        215
                                             220
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Ala Ser Glu Lys
225 230 235 240
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                 245
                                      250
                                                          255
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
             260
                                  265
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
         275
                           280
                                               285
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 310 315 320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325
                                     330
                                                          335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
             340
                                 345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355
                            360
                                                365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                        375
                                             380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                 405
                                     410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                425
                                                     430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435
                           440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
  450
                       455
                                             460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                   470
                                        475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485
490
495
                                    490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515 520 525
Arg Leu Ala Arg Gly His Ser Leu
    530
<210> 314
<211> 312
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<sup>&</sup>lt;212> PRT

<sup>&</sup>lt;213> Artificial Sequence

<sup>&</sup>lt;223> Mutant rep protein: rep40 125 237 600 GCG GCC GCG

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 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
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                                25
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                            40
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
    50
                       55
                                            60
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                    70
                                         75
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
85 90 95
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100
                               105
                                                   110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115 120
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130
                        135
                                            140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                    150
                                        155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165
                                   170
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
            180
                               185
                                                   190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195
                           200
                                                205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
    210
                        215
                                            220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                    230
                                       235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                245
                                   250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
           260
                               265
                                                   270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
       275
                            280
                                                285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
  290
                        295
Arg Leu Ala Arg Gly His Ser Leu
<210> 315
<211> 621
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<213> Artificial Sequence
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Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
          20
                               25
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
                                               45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                       55
                                          60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
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Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 145 150 155 Thr Gln Ala Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ala Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 310 315 320 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys Phe Thr His Gly Gln Lỹs Asp Cys Leu Glu Cys Phe Pro Val Ser Glu

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565
                                       570
  Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 580 585 590
  Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
         595
                              600
                                                   605
  Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                           615
 <210> 316
 <211> 397
 <212> PRT
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 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
            20
                                                       30
 Ser Asn Ala Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                              40
                                                  45
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65 70 75 80
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                85
                                      90
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100
                                 105
                                                       110
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                             120
                                                 125
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                         135 .
                                             140
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                    150
                                         155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165 170 175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
            180
                                 185
                                                      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                             200
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 215 220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                     230
                                         235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                245
                                     250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
275 280 285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                      295
                                              300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 305 310 315 320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                325
                                     330
                                                         335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
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Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln <210> 317 <211> 536 <212> PRT <213> Artificial Sequence <220> <223> Mutant rep protein: rep68 163 259 GCT GCG <400> 317 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Ala Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ala Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp

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355
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Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370
                        375
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385 390 395 400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405
                                     410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
420 425 430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435
                            440
                                                 445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                       455
                                            460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 465 470 475 480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                485
                                     490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
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Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
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Arg Leu Ala Arg Gly His Ser Leu
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<400> 318
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
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                                                    30
Ser Asn Ala Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
       35
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                       55
                                           60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                    70
                                        75
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
               85
                                    90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
           100
                                                    110
                               105
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
       .115
                          120
                                               125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
   130
                       135
                                           140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                   150
                                       155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165 170 175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
           180
                               185
                                                    190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                           200
                                              205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
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Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 230 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 260 265 270 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 275 280 285 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 290 295 Arg Leu Ala Arg Gly His Ser Leu 310 <210> 319 <211> 621 <212> PRT <213> Artificial Sequence <220>

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310
                                          315
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
               325
                                    330
                                                           335
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
             340
                                345
                                                    350
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                         375
     370
                                              380
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                    390
                                         395
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                             440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
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                         455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465 470 480
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                                         475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 510
                                505
                                                      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                             520
                                                 525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
530 540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                    550
                                        555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 565 575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
           580
                                 585
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                            600
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                         615
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<211> 536
<212> PRT
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Ala His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
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                                 25
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
                            40
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                        55
                                            60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                                     90
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Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 110 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Ala Leu 120 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 150 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Ala Ala Gln His 180 185 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 200 195 .205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 270 265 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 310 315 320 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 390 385 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450
460 450 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 510 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 Arg Leu Ala Arg Gly His Ser Leu 530 535

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<sup>&</sup>lt;211> 621

<sup>&</sup>lt;212> PRT

<sup>&</sup>lt;213> Artificial Sequence

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455
                                             460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                   470
                                        475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                485
                                    490
                                                        495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
            500
                                505
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
       515
                           520
                                               525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
530 535 540
    530
                                            540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                   550
                                        555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                565
                                   570
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580 585 590
                               585
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
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Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
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Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
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                      55
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                85
                                    90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
           100
                               105
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
                           120
                                                125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
   130
                        135
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                    150
                                       155
                                                            160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
               165
                                   170
                                                        175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
          180
                                                  190
                               185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ala Asp Gly Asn Ser
                           200
                                               205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                       215
                                           220
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Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln

235

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Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 260 265 270 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 275 280 285 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 290 295 300 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 305 310 315 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 325 330 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 340 345 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 355 360 365 355 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 370 375 380 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln

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<213> Artificial Sequence

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Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 230 235 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala

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245
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
            260
                                265
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Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
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                            280
                                                285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290 . 295 300
                                            300
                       295
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305
                    310
                                         315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
            340
                                345
                                                    350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355
                            360
                                                365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                        375
    370
                                            380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385
                    390
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
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                                    410
                                                        415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ala Asp Gly Asn Ser
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                                425
                                                    430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435
                           440
                                                445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
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   450
                                            460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                   470
                                        475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
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                                                        495
                                    490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
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Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
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Arg Leu Ala Arg Gly His Ser Leu
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
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                                25
                                                   30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                           40
                                               45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                       55
                                           60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                                        95
                85
                                   90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                105
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Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
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Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                        135
                                           140
    130
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                   150
                                       155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                   170
              165
                                                       175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
           180
                               185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ala Asp Gly Asn Ser
                            200
        195
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                       215
                                           220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                   230
                                      235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                                       255
               245
                                   250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                               265
           260
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
        275
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                                               285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
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Arg Leu Ala Arg Gly His Ser Leu
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Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
                           40
Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                       55
                                           60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
           100
                               105
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
       115
                           120
                                               125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly
   130
                      135
                                         140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
                   150
                                      155
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
               165
                                   170
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
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185 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn

180

190

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200
        195
                                                 205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
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                    215
                                           220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
                    230
                                        235
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245 250 255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
            260
                                265
                                                     270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
       275
                         280
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290 295 300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                    310
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335
Thr Ala Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
            340
                               345
                                                     350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                           360
        355
                                                365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370
                        375
                                            380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385 390 395 400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405
                                    410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
           420
                                425
                                                    430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                          440
       435
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
   450
                        455
                                            460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465
                  470
                                        475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
485 490 495
               485
                                    490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                       535
                                            540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                    550
545
                                        555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                565
                                   570
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580 585 590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
      595
                           600
                                                605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
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<sup>&</sup>lt;210> 326

<sup>&</sup>lt;211> 397

<sup>&</sup>lt;212> PRT

<sup>&</sup>lt;213> Artificial Sequence

<sup>&</sup>lt;220>

<sup>&</sup>lt;223> Mutant rep protein: rep52 54 338 495 GCC GCC GCC

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 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
       35
                             40
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                         55
                                              60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                 85
                                     90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100 105 110
Thr Ala Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
        115
                            120
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130 135
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                     150
                                         155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
               165
                                    170
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180 185 190
                                 185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195
                             200
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
    210
                         215
                                              220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                    230
                                        235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 255
                245
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
        275
                             280
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
    290
                        295
                                             300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                    310
                                        315
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 325 330 335
                325
                                     330
                                                         335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
            340
                               345
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
                                                365
                             360
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                        375
                                             380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                    390
                                         395
<210> 327
<211> 536
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep68 54 338 495 GCC GCC GCC
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<400> 327

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Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Ala Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala

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485 🕆
                                     490
                                                           495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                               505
                                                      510
           500
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
        515
                             520
                                                  525
Arg Leu Ala Arg Gly His Ser Leu
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<210> 328
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<213> Artificial Sequence
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<400> 328
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
20 25 30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
35 40 45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
   50
                         55
                                             60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65 70 75 80
                    70
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
85 90 95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
Thr Ala Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115 120 125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
   130
                         135
                                              140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                    150
                                         155
                                                               160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
           - 165
                                    170
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                                     1.90
           180
                                 185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 195 200 205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 215
                        215
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                    230
                                        235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245 250 255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
275 280 285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
  290
                         295
                                              300
Arg Leu Ala Arg Gly His Ser Leu
                    310
<210> 329
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<211> 621 <212> PRT

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<213> Artificial Sequence

<220>
<223> Mutant rep protein: rep78 350 420 GCT GCC

<400> 329 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 25 20 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 60 50 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 105 100 110 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 145 150 155 160 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 190 180 185 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 200 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 270 260 265 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro 340 345 350 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 390 395 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 Ile Val Thr Ala Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 425 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe

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440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
    450
                       455
                                           460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                       475
465
                   470
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
               485
                                    490
                                                        495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                               505
                                                   510
           500
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
       515
                           520
                                               525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
   530
                       535
                                            540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                   550
                                       555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                                   570
                565
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
            580
                               585
                                                   590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                           600
       595
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
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                        615
<210> 330
<211> 397
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<223> Mutant rep protein: rep52 350 420 GCT GCC
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
           20
                                25
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
       35 -
                           40
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                        55
                                            60
   50
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
               85
                                   90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                                   110
           100
                               105
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
                           120
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                                           140
   130
                        135
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                                                            160
                  150
                                      155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                   170
               165
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                                   190
                               185
Ile Val Thr Ala Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                           200
```

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe

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Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 355 360 365 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln

<210> 331 <211> 536 <212> PRT

<213> Artificial Sequence

<223> Mutant rep protein: rep68 350 420 GCT GCC

<400> 331 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys

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240

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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                  250
             245
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
            260
                                265
                                                     270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
        275
                            280
                                               285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
    290
                        295
                                             300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                        315
                   310
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
325 330 335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
            340
                                345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355
                            360
                                                365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                       375
                                           380
    370
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                        395
                    390
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 415
Ile Val Thr Ala Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                            440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450 460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 465 470 480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                                     510
           500
                                505
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
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                           520
Arg Leu Ala Arg Gly His Ser Leu
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                                    30
           20
                               25
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      35
                           40
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55 60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                                        7Š
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
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Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100
                               105
                                                   110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
        115
                           120
                                               125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130
                        135
                                           140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
               165
                                   170
                                                       175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
Ile Val Thr Ala Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195
                                              205
                           200
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                        215
                                           220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                    230
                                       235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                245
                                   250
                                                       255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                               265
                                                  270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
       275
                         280
                                              285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
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                       295
                                            300
Arg Leu Ala Arg Gly His Ser Leu
305
                    310
<210> 333
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<212> PRT
<213> Artificial Sequence
<220>
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Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
          20
                               25
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
       35
                           40
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                       55
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
                   70
                                       75
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                                  90
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
                                                  110
           100
                               105
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
       115
                           120
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
   130
                       135
                                           140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
                   150
                                     155 .
                                                           160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
               165
                                   170
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Ala Ala Gln His
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180
                                 185
Leu Thr His Val Ala Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
       195
                            200
                                                 205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
   210
                      215
                                           220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245 250 255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                                265
           260
                                                     270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
        275
                           280
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290 295 300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                    310
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325
                                    330
                                                         335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                               345
                                                    350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                        375
                                            380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                   390
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                                        415
                405
                                    410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
           420
                               425
                                                    430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435
                                                445
                           440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
   450
                        455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                       475
                    470
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
           500
                               505
Ala Gln Pro Ser Thr Ala Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
       515
                                                525
                           520
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                       535
                                            540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                   550
                                        555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                565
                                  570
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580 585
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
       595
                           600
                                                605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
   610
                        615
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<sup>&</sup>lt;210> 334

<sup>&</sup>lt;211> 397

<sup>&</sup>lt;211> 397 <212> PRT

<sup>&</sup>lt;213> Artificial Sequence

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<220>
<223> Mutant rep protein: rep52 189 197 518 GCG GCG GCA
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           20
                                25
                                                    30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                           40
      35
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
   50
                       55
                                           60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                   70
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
               85
                                    90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                             105
                                                   110
           100
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                           120
                                               125
       115
Phe Tyr Gly Cys Val. Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                        135
                                           140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                    150
                                       155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                   170
                                                        175
               165
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                               185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
       195
                           200
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                                            220
                        215
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245
250
255
               245
                                   250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
       27.5
                           280
Ala Gln Pro Ser Thr Ala Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                                            300
   290
                        295
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                                                            320
                                       315
                   310
305
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 325
               325
                                  330
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 340 345
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
       355
                            360
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                        375
                                           380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                    390
<210> 335
<211> 536
<212> PRT
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<220>

<sup>&</sup>lt;213> Artificial Sequence

-393-

<223> Mutant rep protein: rep68 189 197 518 GCG GCG GCA

<400> 335 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 25 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 40 35 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 145 150 160 150 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 165 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Ala Ala Gln His 185 180 Leu Thr His Val Ala Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 205 200 195 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 245 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 - 280 285 285 275 -280 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 310 315 320 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 335 325 330 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 375 380 370 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 440 445 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 455

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<210> 336 <211> 312

<212> PRT <213> Artificial Sequence

<220>
<223> Mutant rep protein: rep40 189 197 518 GCG GCG GCA

<400> 336 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 10 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 25 30 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 40 35 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 55 60 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 70 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 85 90 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 105 110 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 120 115 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 140 135 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 155 150 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 175 165 170 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 190 180 185 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 205 200 195 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 215 220 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 235 230 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val 245 250 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 260 265 270 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 280 285 Ala Gln Pro Ser Thr Ala Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 295 290 Arg Leu Ala Arg Gly His Ser Leu 310

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<210> 337
<211> 621
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep78 468 516 GCC GCG
<400> 337
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Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
                                                   30
            20
                                25
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
                            40
        35
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                        55
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
                                       75
                    70
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
               85
                                   90
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
                                105
                                                    110
            100
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115 120 125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly
                        135
                                            140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
                   150
                                       155
145
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
                165
                                    170
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
            180
                                185
                                                    190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
                            200
                                                205
        195
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
                       215
                                            220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                                        255
                245
                                    250
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                                265
                                                    270
            260
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                                                285
        275
                           280
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                        295
                                           300
   290
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                       315
                   310
305
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                                        335
                325
                                    330
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
340 345 350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355
                            360
                                                365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                       375
                                           380
  370
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
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Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450. Glu Val Lys Ala Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465 470 480 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val Ala Gln Pro Ala Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 

<210> 338

<211> 397 <212> PRT

<213> Artificial Sequence

<223> Mutant rep protein: rep52 468 516 GCC GCG

<400> 338

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser

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195 200 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 215 220 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 230 235 Glu Val Lys Ala Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 250 245 255 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 260 265 270 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 275 280 285 Ala Gln Pro Ala Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 290 295 300 290 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 310 315 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 325 330 335 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 340 345 350 . Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 355 360 365 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 370 375 380 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 385 390

<210> 339

<211> 536

<212> PRT

<213> Artificial Sequence

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<223> Mutant rep protein: rep68 468 516 GCC GCG

<400> 339

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 10 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 25 30 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 40 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 75 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 90 85 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 110 100 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 145 150 155 160 145 150 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 175 170 165 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 185 190 180 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 200

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Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
    210
                        215
                                            220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
                    230
                                       235
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
               245
                                    250
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
            260
                                265
                                                    270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
       275
                           280
                                               285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                       295
                                           300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                   310
                                       315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325
                                    330 -
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Île Ala His Thr Val Pro
                                                    350
            340
                               345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                           360
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                    390
                                        395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 410 415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
           420
                               425
                                                   430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                          440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
   450
                      455
                                           460
Glu Val Lys Ala Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                   470
                                       475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
           500
                               505
                                                   510
Ala Gln Pro Ala Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                         520
Arg Leu Ala Arg Gly His Ser Leu
   530
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<210> 340

<211> 312

<212> PRT

<213> Artificial Sequence

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<223> Mutant rep protein: rep40 468 516 GCC GCG

<400> 340

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70
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                85
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100
                                105
                                                    110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115
                          120
                                              125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                        135
                                           140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145 150 155
                    150
                                        155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
              165
                                    170
                                                        175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
           180
                                185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
       195
                           200
                                               205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 215 220
   210
                       215
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                                       235
                    230
Glu Val Lys Ala Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
               245
                                   250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                               285
      275
                         280
Ala Gln Pro Ala Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
 290
                       295
                                            300
Arg Leu Ala Arg Gly His Ser Leu
305
<210> 341
<212> PRT
<213> Artificial Sequence
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<211> 621

<220>

<223> Mutant-rep protein: rep78 127 221 350 54 140 GCT GCA GCT GCC GCC

<400> 341 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 30 20 25 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 40 45 Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 110 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Ala Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Ala Ala Gly Gly Gly 135 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys

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145 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 190 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ala Ala Arg Tyr 210 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 250 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 265 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 310 315 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro 345 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 395 390 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 415 410 415 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 425 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
435
440 445 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465 470 475 480 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 505 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 525 525 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 540 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 545 550 560 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 565 570 575 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 580 585 590 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 595 600 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 610

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<211> 397
<212> PRT
<213> Artificial Sequence
<220>
<223> Mutant rep protein: rep52 127 221 350 54 140 GCT
GCA GCT GCC GCC

<400> 342 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 10 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 20 25 30 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 35 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 55 50 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
70 75 80 70 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 90 85 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 105 100 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro 125 120 115 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 140 130 135 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 150 155 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 165 170 175 170 165 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 200 205 195 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 220 210 215 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 235 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 260 265 270 260 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 280 275 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 300 295 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 305 310 315 310 315 305 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 325 330 335 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 340 345 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 365 355 360 The His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 380 375 370 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 390

<210> 343

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<211> 536 <212> PRT

<213> Artificial Sequence

<223> Mutant rep protein: rep68 127 221 350 54 140 GCT GCA GCT GCC GCC

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 1 5 10 15 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 25 30 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 40 35 Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 50 55 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 95 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Ala Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Ala Ala Gly Gly 130 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 145 150 155 160 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 190 185 180 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 205 200 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ala Ala Arg Tyr 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 270 260 265 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285 280 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 320 305 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 330 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro 340 350 345 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 375 380 370 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val

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Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp Arg Leu Ala Arg Gly His Ser Leu 

<210> 344

<211> 312 <212> PRT

<213> Artificial Sequence

<223> Mutant rep protein rep40 127 221 350 54 140 GCT GCA GCT GCC GCC

<400> 344 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 195 200 205 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 260 265 270

WO 03/018820 PCT/IB02/04087

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Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
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                             280
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Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
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Arg Leu Ala Arg Gly His Ser Leu
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20 25 30
                                 25
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
                            40
       35
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                      55
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                85
                                    90
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
            100
                                 105
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
       115
                            120
                                                125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly
                       135
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145 150 155 160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
                                    170
                165
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
                                185
            180
                                                     190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
     195
                            200
                                                205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ala Ala Arg Tyr
  210
                     215
                                           220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225 230 235 240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245 250 255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
           260
                                                    270
                               265
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Ala Gly Gln Gln
                          280
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290 295 300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 310 315 320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335
                                   330
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                                345
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Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
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355
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Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
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                       375
                                            380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                     390
                                         395
385
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 410 415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
            420
                                 425
                                                      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
435
440
445
                           440
       435
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455 460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                 470
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
                485
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
            500
                                505
                                                      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                           520
      515
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 545 550 560
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                 565
                                     570
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580 585 590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
595 600 605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
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                         615
                                              620
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Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
       35
                            40
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Ala Gly Gln Gln 50 55 60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65 70 75 80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
85 90 95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100 105 110
           100
                             105
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115
                           120
                                                125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
```

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Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 150 155 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 175 165 170 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 185 190 180 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 200 205 195 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 215 220 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 230 235 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 255 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 260 265 270 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 275 280 285 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 290 295 300 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 320 305 310 315 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 325 330 335 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 345 340 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 360 365 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 375 380 370 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 390

<210> 347 <211> 536 <212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep68 221 285 GCA GCG

<400> 347

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Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
165 170 175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
            180
                                 185
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
195 200 205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ala Ala Arg Tyr
                       215
                                            220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
                    230
                                       235
                                                              240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245 250 255
               245
                                    250
                                                          255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
260 265 270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Ala Gly Gln Gln
        275
                            280
                                                 285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
  290
                        295
                                             300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                     310
                                         315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
            340
                                                     350
                                345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                             360
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                    390
                                         395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                                     430
            420
                                425
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                           440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450 455 460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                  470
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
           500
                                505
                                                     510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
     515
                            520
Arg Leu Ala Arg Gly His Ser Leu
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                         535
<210> 348
<211> 312
<212> PRT
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
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                                25
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
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                            40
                                                45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Ala Gly Gln Gln
                       55
                                           60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                   70
                                        75
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                105
                                                    110
            100
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                           120
                                                125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130 135 140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                    150
                                       155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                    170
                                                        175
                165
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
            180
                               185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
       195
                           200
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                                           220
    210
                      215
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                    230
                                        235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                245
                                   250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
            260
                               265
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
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                         280
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
  290
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                                            300
Arg Leu Ala Arg Gly His Ser Leu
305
                    310
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<211> 621
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                               25
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
       35
                           40
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                        55
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
                                       75
                   70
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                                   90
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
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		_	100			_		105	_				110		_
		115	Leu				120					125			
	130		Phe			135					140				
Asn 145	Lys	Val	Val	Asp	Glu 150	Cys	Tyr	Ile	Pro	Asn 155	Tyr	Leu	Leu	Pro	Lys 160
	Gln	Pro	Glu	Leu 165	Gln	Trp	Ala	Trp	Thr 170		Met	Glu	Gln	Tyr 175	Leu
Ser	Ala	Cys	Leu 180		Leu	Thr	Glu	Arg 185	Lys	Arg	Leu	Val	Ala 190	Gln	His
Leu	Thr	His 195	Val	Ser	Gln	Thr	Gln 200	Glu	Gln	Asn	Lys	Glu 205	Asn	Gln	Asn
	210		Asp			215					220				
225			Val		230					235					240
			Gln	245					250					255	
			Arg 260					265					270		
		275	Leu				280					285			
	290		Asp			295					300				
305			Asp		310					315					320
			Phe	325					330					335	
			Lys 340					345					350		
		355	Cys				360					365			
	370		Lys			375					380				
385			Glu		390					395					400
			ŗys	405					410					415	
			Ser 420					425					430		
		435	Glu -				440					445			
	450		Arg			455					460				
465			Asp		470					475					480
			Phe	485					490					495	
			Ala 500					505					510		
		515	Ser				520					525			
_	530		Asn			535					540				
545			Arg		550					555					560
			Gly	565					570					575	
Ser	Gln	Pro	Val 580	ser	Val	Val	ŗĀs	Lys 585	Ala	Tyr	GIN	гЛа	ьеи 590	cys	ıyr

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-410-
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
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Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
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Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
       35
                           40
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                        55
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                                        75
                    70
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                                        95
               85
                                    90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                               105
           100
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                          120
                                                125
       115
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                        135
                                            140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                   150
                                        155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                                        175
               165
                                    170
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                               185
           180
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 195 200 205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                       215
   210
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                                       235
                   230
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Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala 265 260 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 275 280 285 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 290 295 300 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 310 315 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 325 330 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 350 345 340 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 365 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp

Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val

250

245

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380
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Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
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                                 25
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
        35
                            40
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                         55
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
                    70
                                         75
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                                                          95 .
               85
                                    90
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
                                                     110
            100
                                105
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115 120 125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
                                                              160
                                        155
                    150
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
165 170 177
               165
                                    170
                                                         175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
                                                     190
                                185
           180
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
195 200 205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
                        215
                                             220
    210
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245 250 255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                                                     270
            260
                                265
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                            280
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                                             300
   290
                        295
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                                              320
                  310
                                        315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
325 330 335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                                 345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
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Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 390 395 385 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 440 435 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala 485 490 495 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 510 500 505 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 Arg Leu Ala Arg Gly His Ser Leu 530

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<213> Artificial Sequence

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Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala 260

Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 275

Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 290

Arg Leu Ala Arg Gly His Ser Leu 305

<210> 353
<211> 621.

<212> PRT

<213> Artificial Sequence

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325
                                           330
  Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345
   Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
355 360 365
                                  360
                                                        365
   Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
       370
                            375
                                                  380
  Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385 390 395 400
  Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 415
   Ile Val Thr Ala Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
420 425 430
                                     425
                                                            430
  Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 445
  Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450 455 460
  Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 465 470 475 480
                                             475
  Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                     505
                                                           510
  Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
           515
                                520
                                                      525
  Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 540
  Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 545 550 555
  Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
565 570 575
  Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 580 585 590
  Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
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                                600
  Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
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<211> 397

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep52 20 54 420 495 GCC GCC GCC

<400> 354

 Met
 Glu
 Leu
 Val
 Gly
 Trp
 Leu
 Val
 Asp
 Lys
 Gly
 Ile
 Thr
 Lys
 Glu
 Lys
 Lys
 Lys
 Gly
 Ile
 Thr
 Ser
 Glu
 Lys
 Lys
 Lys
 Ile
 Ser
 Phe
 Asn
 Ala
 Ala</th

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100
                                  105
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
       115
                             120
                                                   125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                         135
                                              140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                    150
                                         155
                                                                160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                 165
                                      170
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180 185 190
Ile Val Thr Ala Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195
                             200
                                                   205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 220
                        215
                                              220
    210
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                     230
                                          235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245 250 255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                           280
                                                  285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290 295 300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 305 310 315 320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 325 330 335
                 325
                                     330
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                                                      350
             340
                                 345
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
355 360 365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 370 375 380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
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<213> Artificial Sequence

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100
                                 105
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115 120 125
      115
                             120
                                                 125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly
                        135
                                            140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
                 150
                                        155
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
                165
                                     170
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
           180
                               185
                                                     190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
                                                 205
      195
                            200
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
                      215
                                            220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                                                     270
            260
                                265
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285
        275
                          280
                                                285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                   310
                                         315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335
                                                          335
                                    330
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
       355
                            360
                                                365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
370 380
                                           380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385 390 395 400
                   390
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
               405
                                    410
Ile Val Thr Ala Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                                     430
           420
                                425
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
435
440
                           440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                  470
                                        475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
           500
                                505
                                                     510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
     515
                           520
Arg Leu Ala Arg Gly His Ser Leu
                        535
   530
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<sup>&</sup>lt;210> 356

<sup>&</sup>lt;211> 312

<sup>&</sup>lt;212> PRT

<sup>&</sup>lt;213> Artificial Sequence

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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
            20
                                  25
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                             40
                                                  45
        35
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                        55
                                             60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80
                    70
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
85 90 95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100
                                 105
                                                     110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115 120 125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                        135
                                             140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                    150
                                        155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165 170 175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                 185
            180
Ile Val Thr Ala Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                                  205
        195
                             200
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
    210
                        215
                                             220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 235
                    230
                                        235
225
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245 250 255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                            280
        275
                                                  285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
  290
                        295
Arg Leu Ala Arg Gly His Ser Leu
30Š
                     310
<210> 357
<211> 621
<212> PRT
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Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
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                                     10
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
                                                      30
            20
                                 25
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
35 40 45
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Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Ala Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu

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535
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                  550
                                     555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                                 570
               565
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
           580
                              585
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                          600
       595
Leu Val Asn Ala Asp Leu Asp Asp Cys Ile Phe Glu Gln
                       615
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
           20
                              25
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                           40
       35
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                                      75
                  70
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                  90
               85
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                          120
       115
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                                           140
                       135
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                                                           160
                  150
                                      155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                  170
                                                      175
              165
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Ala Pro Thr Pro Val
                               185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                           200
       1.95
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                                           220
                     · 215
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                  230
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                         280
       275
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                      295
                                          300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
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```
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                                   330
               325
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                               345
                                                   350
           340
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
                           360
                                               365
       355
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                       375
                                           380
 370
Leu Val Asn Ala Asp Leu Asp Asp Cys Ile Phe Glu Gln
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385
<210> 359 -
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50 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 105 100 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 125 120 115 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly 130 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
150
155
160 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 170 165 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 205 200 195 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 265 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala

175

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325
                                    330
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                               345
                                                   350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355
       355
                                              365
                            360
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                                           380
                        375
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                   390
                                       395
385
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Ala Pro Thr Pro Val
                                                        415
                                   410
               405
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                               425
                                                    430
           420
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                                               445
        435
                           440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450 455 460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                       475
                   470
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490
               485
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                              505
                                                    510
           500
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515 520 525
Arg Leu Ala Arg Gly His Ser Leu
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                                                    30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                           40
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                       55
                                           60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
               85
                                    90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                              105
                                                   110
           100
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                                               125
                           120
        115
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130 135 140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                                       155
                   150
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
```

170

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Ala Pro Thr Pro Val 185

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Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                            200
        195
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
    210
                        215
                                            220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                    230
                                       235
225
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                245
                                    250
                                                        255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                               265
           260
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                         280
                                               285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                       295
   290
Arg Leu Ala Arg Gly His Ser Leu
                    310
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<400> 361
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Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
                                25
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                       55
   50
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
                   70
                                        75
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                                  90
               85
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
                                                    110
            100
                                105
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
                                                125
                            120
       115
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly
                                            140
   130
                        135
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
                   150
                                                            160
                                       155
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
                                    170
               165
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
                                                    190
                                185
           180
Leu Thr His Val Ala Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
                                                205
       195
                            200
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
                      215
                                            220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225 230 235 240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245 250 255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
```

265 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln

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285

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Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290 295 300
    290
                        295
                                             300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305
                    310
                                        315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
              325
                                   330
                                                         335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
            340
                               345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                            360
        355
                                                 365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                        375
                                            380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                       395
                 390
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Ala Pro Thr Pro Val
               405
                                    410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
       435.
                                                445
                            440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
   450
                       455
                                            460 ·
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 465 470 475 480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
               485
                                                        495
                                    490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515 520 525
                            520
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 540
                      535
                                            540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
545 550 560
                                                            560
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                                                        575
                565
                                    570
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
            580
                                585
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
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                           600
                                                605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                25
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
       35
                           40
                                                45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
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Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                    90
                85
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                105
                                                    110
           100
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                                                125
                           120
        115
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
   130
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                    150
                                        155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
               165
                                    170
                                                        175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Ala Pro Thr Pro Val
                               185
           180
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195
                            200
                                                205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                                            220
                        215
   210
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                    230
                                        235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                                        255
               245
                                   250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                                285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                        295
                                            300
   290
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                    310
                                        315
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                                                        335
               325
                                   330
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                                                   350
           340
                                345
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
355 360 365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                                            380
  370
                        375
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                    390
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<210> 363

<211> 536

<212> PRT

<213> Artificial Sequence

220>

<223> Mutant rep protein: rep68 197 412 GCG GCC

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Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 105 110 100 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 140 135 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 145 150 155 160 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 Leu Thr His Val Ala Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 205 200 195 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 215 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 245 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 270 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
275
280
285 280 275 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 295 290 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 310 315 310 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 340 345 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 380 375 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400 390 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Ala Pro Thr Pro Val 405 410 415 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 445 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 510 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 525 Arg Leu Ala Arg Gly His Ser Leu

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<211> 312
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep40 197 412 GCG GCC
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
       35
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                                            60
                        55
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                                        75
                   70
65
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                    90
                85
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                                   110
                                105
           100
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                           120
                                                125
       115
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                                            140
                        135
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                                                            160
                    150
                                        155
145
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                    170
                                                        175
               165
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Ala Pro Thr Pro Val
                                185
            180
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                            200
                                                205
       195
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                                            220
                        215
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                                                            240
                                       235
                    230
225
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                    250
                245
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                                                   270
                              . 265
           260
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                            280
                                                285
       275
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                                            300
 290
                        295
Arg Leu Ala Arg Gly His Ser Leu
                    310
305
<210> 365
<211> 621
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep78 412 495 511 GCC GCC GCA
Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
                                    10
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
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25 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 40 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 50 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 135 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 150 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 170 165 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 185 180 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 270 260 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 285 275 280 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 295 290 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 365 355

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 360 380 375 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 390 395 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Ala Pro Thr Pro Val 405 410 415 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 440 435 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala 485 490 495 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ala Val 505

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Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 

<210> 366 <211> 397

<211> 397 <212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep52 412 495 511 GCC GCC GCA

<400> 366 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 150 . Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Ala Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ala Val Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp

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295
                                             300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 305
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                325
                                     330
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                                345
            340
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
       355
                            360
                                                 365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                                            380
                       375
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                    390
<210> 367
<211> 536
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep68 412 495 511 GCC GCC GCA
<400> 367
Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
                                 25
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
                            40
                                                 45
       35
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                        55
                                            60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                                    90
                85
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
                                105
                                                     110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115 120 125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly
                                            140
                        135
  . 130
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145 150 155 160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
                                     170
                165
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
                                185
                                                     190
           180
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
        195
                            200
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
   210
                        215
                                            220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225 230 240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
               245
                                    250
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                                               285
                             280
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
```

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Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 310 320 305 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 335 325 330 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 350 345 340 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 375 380 370 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 395 390 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Ala Pro Thr Pro Val 405 410 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 425 420 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 440 445 435 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 475 470 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
485 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ala Val 510 505 500 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 520 515 Arg Leu Ala Arg Gly His Ser Leu 535 530

<210> 368 <211> 312 <212> PRT <213> Artificial Sequence

<220>
<223> Mutant rep protein: rep40 412 495 511 GCC GCC GCA

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 20 25 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 40 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 60 55 50 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 70 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 95 85 90 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 110 100 105 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 120 125 115 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 130 135 140 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 150 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg

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175 170 165 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Ala Pro Thr Pro Val 180 185 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 200 205 195 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 215 220 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 235 240 230 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 255 245 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala 260 265 270 260 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ala Val 280 275 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 295 Arg Leu Ala Arg Gly His Ser Leu 310 305 <210> 369 <211> 621 <212> PRT <213> Artificial Sequence <223> Mutant rep protein: rep78 98 422 GCC GCC Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 10 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 25. 30 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 40 45 35 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Ala Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 110 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 125 120 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly 130 135 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145 150 155 160 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170

Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 185

Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn

Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala

205

235

200

215

230

180

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Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                               265
           260
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                           280
                                               285
       275
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                       295
                                           300
   290
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                       315
                                                           320
                   310
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                   330
                                                       335
               325
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
           340
                               345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                           360
                                              365
       355
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                       375
                                          380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                   390
                                       395
385
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
               405
                                   410
Ile Val Thr Ser Asn Ala Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                                   430
                               425
          420
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                           440
       435
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                                           460
                       455
   450
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                   470
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                                   490
               485
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
           500
                               505
                                                   510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                                              525
                           520
       515
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                                           540
                       535
   530
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                                       555
                                                           560
                   550
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                                                       575
               565
                                   570
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
                              585
                                                   590
           580
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                                               605
                           600
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
   610
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<sup>&</sup>lt;210> 370 <211> 397

<sup>&</sup>lt;212> PRT <213> Artificial Sequence

<sup>&</sup>lt;220> <223> Mutant rep protein: rep52 98 422 GCC GCC

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Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
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                         55
    50
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
85 90 95
                85
                                    90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100
                                105
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                            120
                                                  125
       -115
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                                              140
                         135
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                    150
                                         155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165 170 175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
            180
                                 185
                                                      190
Ile Val Thr Ser Asn Ala Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                                  205
        195
                             200
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                        215
                                              220
  210
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245 250 255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                                  285
        275
                             280
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                        295
                                              300
  290
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 305 310 315 320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
325 330 335
                 325
                                      330
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
            340
                                 345
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
355 360 365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 370 380
                         375
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                     390
                                          395
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<210> 371

<211> 536 <212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep68 98 422 GCC GCC

### -434-

Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Ala Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His . 180 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 270 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg . 395 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Ala Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 465 470 475 480 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp Arg Leu Ala Arg Gly His Ser Leu

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535
    530
<210> 372
<211> 312
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep40 98 422 GCC GCC
<400> 372
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                                    30
            20
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
        35
                           40
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                        55
                                            60
   50
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80
                    70
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
               85
                                    90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                                    110
            100
                                105
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                           120
        115
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                                            140
                        135
    130
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                                                             160
                    150
                                        155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                    170
                                                         175
               165
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                                   190
            180
                                185
Ile Val Thr Ser Asn Ala Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                                205
                            200
        195
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
    210
                       215
                                            220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                   230
                                       235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                   250
                245
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                            280
        275
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
  290
                        295
Arg Leu Ala Arg Gly His Ser Leu
                    310
305
<210> 373
<211> 621
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep78 17 127 189 GCG GCT GCG
<400> 373
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Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 10 Ala His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 25 30 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 45 40 35 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 70 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 105 100 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Ala Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 140 135 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 150 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Ala Ala Gln His 180 185 190 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 200 195 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 220 215 210 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 236 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 270 265 260 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 300 295 290 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 310 315 320 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 345 340 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 365 360 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 375 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 395 390 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 425 420 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450
455 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 475 470 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala

## -437-

485 490 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 505 510 500 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515 520 525 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 535 540 530 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 555 550 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 565 570 575 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 580 590 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 600 605 595 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 615 . <210> 374 <211> 536 <212> PRT <213> Artificial Sequence <223> Mutant rep protein: rep68 17 127 189 GCG GCT GCG <400> 374 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 10 Ala His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu . 30 25 20 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 40 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 50 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 90 85 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 110 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Ala Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 135 130 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 155 150 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Ala Ala Gln His 185 180 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 265

### -438-

Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 280 285 275 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 295 300 290 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 310 315 305 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 330 335 325 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 350 340 345 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 360 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 375 380 370 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 390 395 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 425 430 420 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 440 435 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 455 460 450 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 475 470 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 505 510 500 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 520 515 Arg Leu Ala Arg Gly His Ser Leu

<210> 375 <211> 621 <212> PRT

<213> Artificial Sequence

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# -439-

							_								
Acr	130		1 1/2	1 7 ~~		13:		7		_	140		_	_	,
145	. шуг	va.	L va.	LASI	150	ı Cy	s ту	c TT	e Pro	o Ası 15!		r Lei	ı Let	1 Pro	Lys
		Pro	Gl:	1 Let 165	ı Glı		p Ala	a Tr	7 Th:	r Ası	n Met	: Glı	ı Glr	1 Tyr	160 Leu
Ser	Ala	су Су	Let 180	ı Ası		ı Thi	r Glı	1 Arg	J Lys	5 Arg	J Let	ı Val	l Ala 190	Glr	His
		TAP	>				200	ı Glı	ı Glr			205	ı Asr	Glr	Asn
	210	1				215	5				220	: Ser	: Ala		Tyr
225					230	,				235	5				Lys 240
				245					250	)				255	Ala
			260					265	5				270	Gly	_
		275					280	1				285	١,		Gln
	290					295	5				300			Glu	
305	GTĀ	TYT	Asp	Pro	310	Tyr	. ATa	. Ala	Ser	Val 315	Phe	Leu	Gly	Trp	Ala 320
				325	Lys	Arg			330	Trp	Leu			Pro 335	Ala
			340					345	Ala	Ile			350	Val	
		355					360					365		Asn	
	3/0					- 375					380			Thr	
385					390					395				Val	400
				405					410					Pro 415	
			420					425					430	Asn Lys	
		435	-				440					445		Lys	
	450					455					460			Glu	
465					470					475					480
				485					490					Ala 495	
			500					505					510	Ser	
Ala		272					520					525			
	530					535					540				
Phe 545 Phe					550					555					560
				565					570					575	
Ser (			580					585					590		
Ile I		595					600					605	AIa	Cys	Asp
Leu 1	Val . 510	ASN	val	ASP :		Asp 615	Asp	Cys	īle	Phe	Glu 620	Gln			

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<211> 397
<212> PRT
<213> Artificial Sequence
<220>
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
         20
                                 25
                                                    30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
35 40 45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
   50
                        55
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80
                    70
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
               85
                                    90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                               105
                                                    110
           100
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                           120
                                                125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130
                        135
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                                       155
                    150
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
               165
                                   170
                                                        175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180 185
Ile Val Thr Ser Asn Thr Asn Met, Cys Ala Val Ile Asp Gly Asn Ser
                                                205
        195
                            200
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                                            220
    210
                        215
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                                                             240
                                       235
225
                    230
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
               245
                                   250
                                                        255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                            280
                                                285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
    290
                        295
                                            300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                                                             320
                   310
                                        315
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
325 330 335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                                                   350
           340
                                345
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
       355
                            360
                                                365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                        375
                                            380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385
                    390
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<210> 377

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<211> 536 <212> PRT <213> Artificial Sequence <223> Mutant rep protein: rep68 20 54 495 GCC GCC GCC <400> 377 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Ala Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 25 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 40 Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 60 50 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 70 75 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 90 85 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 110 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 120 115 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 140 135 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 155 150 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 185 190 180 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 200 205 195 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 220 215 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 235 230 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 250 245 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 285 280 275 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 315 310 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 335 325 330 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 375 370 . Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385 390 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser

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420 425 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 440 445 435 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 460 455 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala 495 485 490 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 505 510 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 525 Arg Leu Ala Arg Gly His Ser Leu <210> 378 <211> 312 <212> PRT <213> Artificial Sequence <220> <223> Mutant rep protein: rep40 20 54 495 GCC GCC GCC <400> 378 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 20 3.0 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 40 35 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 55 60 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 85 90 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 125 120 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 130 135 140 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 150 155 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 165 170 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 180 185 190 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 195 200 205 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 225 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 230 235 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 255 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala 260 . 265 270

Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val

### -443-

Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp Arg Leu Ala Arg Gly His Ser Leu <210> 379 <211> 621 <212> PRT <213> Artificial Sequence <223> Mutant rep protein: rep78 259 54 GCG GCC <400> 379 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ala Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala

### -444-

```
375
                                             380
    370
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                       395
              390
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                   410
               405
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                           440
       435
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                       455
                                            460
  450
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465 470 480
                  470
                                        475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
               485
                                    490
                                                        495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515 520 525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                      535
                                            540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 545 550 560
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                565
                                   570
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580 585 590
                               585
           580
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                           600
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                        615
   610
<210> 380
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Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
                                    10
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
           20
Ser Asn Ala Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                           40
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                       55
  50
                                            60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 85 90 95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
           100
                               105
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                           120
                                                125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                       135
                                           140
  130
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
```

150

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Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 175 170 165 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 180 185 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 205 200 195 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 220 215 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 230 235 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 255 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 265 260 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 285 280 275 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 300 290 295 . Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 305 310 315 320 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 325 330 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 345 340 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 365 360 355 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 375 380 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 390 385 <210> 381 <211> 536 <212> PRT

<213> Artificial Sequence

<223> Mutant rep protein: rep68 259 54 GCG GCC

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 25 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 45 35 40 Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 60 50 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 75 70 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 110 100 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 140 135 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu

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```
165
                                      170
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
                                 185
                                                       190
           180
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
195 200 205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
                         215
                                             220
   210
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225 230 235 240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245 250 255
                245
                                     250
Ser Asn Ala Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                                 265
                                                      270
          260
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
  290
                         295
                                              300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                                                320
                     310
                                          315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                                345
            340
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                                              380
                         375
   370
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                    390
                                         395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                             440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 460
                         455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                    470
                                         475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
       515
                             520
Arg Leu Ala Arg Gly His Ser Leu
   530
                         535
<210> 382
<211> 312
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep40 259 54 GCG GCC
<400> 382
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
                                      10
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
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Ser Asn Ala Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                            40
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                        55
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                    70
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
               85
                                    90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
           100
                              105
                                                   110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                           120
                                               125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
   130
                       135
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                   150
                                       155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
               165
                                   170
                                                       175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
          180
                              185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                               205
       195
                           200
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                                           220
                        215
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                   230
                                       235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                   250
               245
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
          260
                                                   270
                               265
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
       275
                                               285
                           280
Ala Gin Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
  290
                       295
                                           300
Arg Leu Ala Arg Gly His Ser Leu
305
                   310
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<210> 383 <211> 621

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep78 335 399 GCT GCG

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								•							
		115					120					125			
Pro	Asn 130	Trp	Phe	Ala	Val	Thr 135	Lys	Thr	Arg	Asn	Gly 140	Ala	Gly	Gly	Gly
Asn 145	Lys	Val	Val	Asp	Glu 150		Tyr	Ile	Pro	Asn 155	Tyr	Leu	Leu	Pro	Lys 160
Thr	Gln	Pro	Glu	Leu 165	Gln	Trp	Ala	Trp	Thr 170	Asn	Met	Glu	Gln	Tyr 175	Leu
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg 185	Lys	Arg	Leu	Val	Ala 190		His
Leu	Thr		180 Val	Ser	Gln	Thr	Gln 200		Gln	Asn	Lys	Glu 205		Gln	Asn
Pro		195 Ser	qaA	Ala	Pro		Ile	Arg	Ser	Lys	Thr 220		Ala	Arg	Tyr
	210 Glu	Leu	Val	Gly	Trp	215 Leu	Val	Asp	Lys	Gly 235		Thr	Ser	Glu	Lys 240
225 Gln	Trp	Ile	Gln	Glu	230 Asp	Gln	Ala	Ser	Tyr 250	Ile	Ser	Phe	Asn	Ala 255	
Ser	Asn	Ser		245 Ser	Gln	Ile	Lys	Ala 265	Ala	Leu	Asp	Asn	Ala 270		Lys
Ile	Met	Ser 275	260 Leu	Thr	Lys	Thr	Ala 280	Pro	Asp	Tyr	Leu	Val 285		Gln	Gln
	290	Glu		Ile		295	Asn				300				
305	Gly			Pro	310	Tyr				315					320
Thr				Gly 325					330					333	
			340	Thr				345					350		
		355		Val			360					365			
	370	Asp		Met		375	Trp				380				
3 8 5	Val			Ser	390					395					400
				Cys 405					410					413	
			420	Asn				425					430		
		435		His			440					445			
	450			Arg		455					460				
465				Phe	470					4/5					400
				Tyr 485					490					423	
			500	Asp				505					210		
		515		Thr			520					525			
	530					535					540				Leu
545				Gln	550					555					200
				Gln 565					570					<b>5/</b> 3	
			580	Ser				585					590		
Ile	His	His 595	Ile	Met	Gly	Lys	Val 600	Pro	Asp	Ala	Cys	Thr 605	ATA	cys	Asp

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Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
<210> 384
<211> 397
<212> PRT
<213> Artificial Sequence
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
            20
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                           40
       35
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                       55
                                           60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
70 75 80
                  70
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                    90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Ala Ala
                                                    110
                               105
           100
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                                                125
                            120
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130 135 140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                    150
                                       155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Ala Arg
                165
                                    170
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                                205
                            200
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                       215
                                           220
   210
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                                       235
                    230
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 255
                245
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
            260
                               265
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                                285
                           280
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                     · 295
                                           300
   290
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                    310
                                        315
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                                    330
                325
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                                                   350
            340
                                345
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
355 360 365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                        375
                                            380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
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385 390 395 <210> 385 <211> 536 <212> PRT <213> Artificial Sequence <223> Mutant rep protein: rep68 335 399 GCT GCG Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 25 30 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 40 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 50 55 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 110 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 120 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140 130 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 145 150 155 160 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 190 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 220 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240 235 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 270 260 265 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Ala Ala 325 330 335 330 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 350 340 345 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Ala Arg

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Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 430 420 425 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 440 445 435 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 460 450 455 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 505 510 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 520 515 Arg Leu Ala Arg Gly His Ser Leu 535

<210> 386

<211> 312

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep40 335 399 GCT GCG

<400> 386 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 10 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 20 25 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 35 40 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 60 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 90 85 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Ala Ala 100 105 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 120 115 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 140 135 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 150 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Ala Arg 170 165 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 190 180 185 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 205 195 200 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 215 220 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 235 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala

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260
                                265
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                                285
                          280
      275
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                       295
   290
Arg Leu Ala Arg Gly His Ser Leu
                    310
305
<210> 387
<211> 621
<212> PRT
<213> Artificial Sequence
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<400> 387
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                                    10
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
                                                   30
                               25
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
                           40
       35
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                        55
    50
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65 70 75 80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                                   90
               85
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
                                                   110
                               105
           100
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115 120 125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly
                                           140
                        135
   130
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
                                                            160
                                       155
145
                    150
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
              165
                                    170
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
                               185
           180
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
                                               205
                            200
        195
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ala Ala Arg Tyr
                        215
                                            220
    210
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
                                       235
                                                            240
                    230
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
               245
                                  250
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                                                   270
                               265
           260
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                                              285
                            280
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290 295 300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                        315
                    310
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                                        335
                                   330
               325
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                                345
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```
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
       355
                            360
                                               365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                                            380
   370
                        375
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                        395
                   390
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
               405
                                   410
                                                        415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ala
                              425
           420
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                            440
       435
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450
460
                       455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                       475
                   470
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
               485
                                   490
                                                        495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                               505
           500
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                                               525
                           520
       515
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                                            540
                       535
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                   550
                                       555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                                  570
               565
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580 585 590
           580
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
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                           600
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                        615
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<210> 388

<211> 397 <212> PRT

<213> Artificial Sequence

<223> Mutant rep protein: rep52 221 432 GCA GCA

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130
                         135
                                              140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                     150
                                        155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165
                                                         175
                                     170
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
            180
                                 185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ala
                            200
                                                205
       195
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                        215
                                             220
    210
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 255
                245
                                     250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
        275
                             280
                                                 285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                                             300
    290
                         295
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305
                    310
                                         315
                                                              320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                325
                                    330
                                                          335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 340 345 350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
355 360 365
                             360
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                         375
                                            380
  370
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                     390
385
<210> 389
<211> 536
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep68 221 432 GCA GCA
<400> 389
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Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
20 25 30
                                 25
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
                            40
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                        55
   50
                                             60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 80
                                        75
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
               85
                                    90 .
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
            100
                                105
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
       115
                            120
                                                 125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
```

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Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
                   150
                                       155
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
                                                        175
                                   170
               165
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
                                                   190
                               185
           180
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
                            200
       195
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ala Ala Arg Tyr
                                           220
   210
                       215
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                   250
                245
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                                                   270
           260
                                265
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                           280
       275
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                       295
                                            300
  290
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                                            320
                                       315
                   310
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                                        335
                                   330
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                                                    350
                                345
           340
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                                                365
                            360
       355
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                                           380
                       375
    37Ô
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                   390
                                       395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405
                                   410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ala
                                                   430
                                425
           420
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                                                445
                           440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                       455
                                            460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                       475 .
                  470
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                                    490
                485
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                                   510
           500
                               505
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                           520
      515
Arg Leu Ala Arg Gly His Ser Leu
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    530
<210> 390
<211> 312
<212> PRT
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<sup>&</sup>lt;220>
<223> Mutant rep protein: rep40 221 432 GCA GCA

<sup>&</sup>lt;400> 390 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys

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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
           20
                                25
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                            40
       35
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                        55
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                    70
65
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                    90
                85
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                                     110
                                105
           100
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                           120
       115
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130 140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                    150
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                    170
                165
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
           180 .
                               185
                                                    190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ala
195 200 205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                                            220
                        215
   210
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                    230
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                           280
                                                 285
       275
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                                             300
                        295
Arg Leu Ala Arg Gly His Ser Leu
305
<210> 391
<211> 621
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep78 259 516 GCG GCG
<400> 391
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                                    10
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
20 25 30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
                            40
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                        55
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
                                        75
                   70
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
```

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Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr Hìs Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ala Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 495 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val Ala Gln Pro Ala Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 540 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 545 550 560 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr

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580
                                 585
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
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      595
                            600
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
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Ser Asn Ala Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                                                 45
                            40
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                       55
                                            60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65 70 75 80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                85
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                 105
            100
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                                                 125
       115
                            120
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130 135 140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145 150 155 160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165
                                     170
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
            180
                                 185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
       195
                           200
                                                 205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 215 220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val
                245
                                    250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                                 285
       275
                           280
Ala Gln Pro Ala Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290 295 300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 305 310 315 320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                                     330
                325
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                                                     350
            340
                               345
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
                             360
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Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
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   370
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
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Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
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                                                  30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
       35
                           40
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                       55
   50
Thr Glu Trp Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
                   70
                                       75
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
               85
                                   90
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
                              105
                                                   110
           100
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
                                              125
                           120
       115
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly
                       135
                                          140
  130
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
                                      155
                                                           160
                   150
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
                                                      175
                                   170
              165
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
                              185
                                                   190
           180
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
                                              205
       195
                           200
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
                       215
   210
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
                   230
                                      235
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                                       255
                                  250
               245
Ser Asn Ala Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                              265
           260
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                                               285
        275
                           280
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                       295
                                           300
   290
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                       315
                  310
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                  330
                                                       335
                325
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                                                  350
                               345
            340
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                           360
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
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375
    370
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                                            400
                  390
                                        395
385
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                   410
               405
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                               425
           420
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                           440
        435
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                       455
                                           460
   450
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                       475
                  470
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
               485
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                505
Ala Gln Pro Ala Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                            520
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Arg Leu Ala Arg Gly His Ser Leu
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
           20
Ser Asn Ala Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
35 40 45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                      55
                                            60
   50
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                    90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                105
            100
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                                                125
                            120
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130 135 140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                                       155
                    150
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165 170 175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                185
            180
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                                205
       195
                           200
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                       215
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225 230 235 240
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Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                     250
               245
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 . 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
        275
                            280
                                                 285
Ala Gln Pro Ala Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                        295
   290
Arg Leu Ala Arg Gly His Ser Leu
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Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
                                 25
                                                     30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
                            40
        35
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                        55
                                             60
    50
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
                    70
                                         75
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                                    90
                85
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
            100
                                 105
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115 120 125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly 130
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
                    150
                                        1.55
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
165 170 175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
            180
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
                            200
                                                 205
       195
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215' 220
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 250 245 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 285 275 280 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 310 315

Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235

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325
                                                           335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
            340
                                 345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                       375
    370
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385 390 395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                     410
                                                           415
                405
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                 425
                                                      430
           420
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
435 440 445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450 460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465 470 480
                                         475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
485 490 495
                485
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
         500
                                505
Ala Gln Pro Ala Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515 520 525
        515
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                                              540
                        535
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 545 550 555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                                    570
                565
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580 585
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                            600
       595
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                         615
<210> 396
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                                      30
           20
                                 25
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                            40
        35
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
50 60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                     90
                85
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                 105
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Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
        115
                             120
                                                 125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130
                         135
                                             140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                   150 ·
                                       155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165 170 175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
            180
                                 185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195
                             200
                                                 205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                       215
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                245
                                    250
                                                        255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
            260
                                 265
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
        275
                            280
Ala Gln Pro Ala Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                      295
    290
                                          300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 305 310 315 320
                                                             320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 325 330 335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 340 345 350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
        355
                            360
                                                365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                        375
                                           380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385
                    390
<210> 397
<211> 536
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Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                       55
   50
                                           60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
               85
                                   90
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
            100
                                105
                                                     110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
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115
                             120
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly
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                        135
                                           140
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
                    150
                                         155
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
                                     170
                                                         175
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
             180
                                 185
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
        195
                            200
                                                205
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 220
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
                    230
                                       235
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245
                 245
                                    250
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
            260
                                265
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
        275
                           280
                                              285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                    310
                                        315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                 325
                                    330
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370
                        375
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                    390
                                        395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405
                                    410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
       435
                           440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                   470
                                        475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
485 490 495
                                   490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
           500
                               505
                                                   510
Ala Gln Pro Ala Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
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                           520
Arg Leu Ala Arg Gly His Ser Leu
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<210> 398
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<212> PRT
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<223> Mutant rep protein: rep40 495 516 GCC GCG

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Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 235 240 Gin Trp Ile Gin Glu Asp Gin Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Ala Pro Val 405 415 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515 520 525 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 540 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu

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```
565
                                       570
  Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
             580
                                  585
                                                       590
  Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
         595
                             600
  Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
     610
                          615
  <210> 400
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 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
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                                  25
                                                     30
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
         35
                             40
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                         55
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65 70 75 80
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                 85
                                      90
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
             100
                                 105
                                                     110
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
        115
                            120
                                                  125
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130
                         135
                                              140
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
150 155 160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                 165
                                     170
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Ala Pro Val
                                185
                                                    190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195 200 205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
   210
                        215
                                             220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                    230
                                        235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                245
                                    250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
275 280 285
                                                 285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                       295
                                             300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                   310
                                        315
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                325
                                   330
                                                        335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                                345
                                                     350
```

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Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 355 360 365 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 370 375 380 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 390 <210> 401 <211> 536 <212> PRT <213> Artificial Sequence <223> Mutant rep protein: rep68 414 14 GCT GCC <400> 401 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Ala Leu Asp 10 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 25 30 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 40 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 50 55 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 70 75 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 110 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 150 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 190 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 255 250 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 270 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 280 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 345 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp

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360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 390 395 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Ala Pro Val 405 410 415 410 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 -455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 495 490 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 505 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 Arg Leu Ala Arg Gly His Ser Leu 530 535

<210> 402 <211> 312

<212> PRT <213> Artificial Sequence

<220>

<223> Mutant rep protein: rep40 414 14 GCT GCC

<400> 402 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 20 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 40 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55 60 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 85 90 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 100 105 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 115 120 125 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 130 135 140 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 150 155 160 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 175 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Ala Pro Val 180 185 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 200 205 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 215

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Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 230 235 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 250 245 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 270 265 260 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 280 285 275 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 295 290 Arg Leu Ala Arg Gly His Ser Leu 310 305

<210> 403 <211> 621

<212> PRT

<213> Artificial Sequence

<220>
<223> Mutant rep protein: rep78 74 402 495 GCG GCC GCC

<400> 403 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 25 20 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 45 40 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 60 50 Thr Glu Trp Arg Arg Val Ser Lys Ala Ala Glu Ala Leu Phe Phe Val 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 95 85 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 105 100 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 155 150 145 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 170 165 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 185 180 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 205 200 195 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 220 215 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 230 225 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 250 255 245 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 270 260 265 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 300 295 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala

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```
320
                                          315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                     310
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                                 345
            340
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                                                  365
                            360.
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                       375
                                              380
   370
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385 390 395 400
Val Ala Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 410 415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                425
           420
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                             440
       435
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                                             460
                       455
 450
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465 470 475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                 505
            500
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                                                  525
                             520
       515
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 545 550 555 560
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 565 570 575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
                                 585
            580
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                            600
                                                  605
       595
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                         615
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<210> 404 <211> 397

<212> PRT

<213> Artificial Sequence

<220>
<223> Mutant rep protein: rep52 74 402 495 GCG GCC GCC

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Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                              105
           100
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                                               125
                           120
       115
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                       135
                                          140
   130
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                                       155
                    150
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
               165
                                   170
Val Ala Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
           180
                               185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                               205
                           200
       195
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                                           220
                        215
   210
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                                                            240
                    230
                                       235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
               245
                                   250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
                               265
           260
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                               285
                         280
        275
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                                          300
                       295
   290
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                    310
                                       315
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                                   330
               325
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                               345
           340
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
                                              365
                            360
       355
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 370 375 380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                    390
<210> 405
<211> 536
<212> PRT
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<213> Artificial Sequence

<223> Mutant rep protein: rep68 74 402 495 GCG GCC GCC

<400> 405 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 10 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 25 20 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 45 40 35 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 Thr Glu Trp Arg Arg Val Ser Lys Ala Ala Glu Ala Leu Phe Phe Val 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 90 85 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile

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105
             100
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115 120 125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
                                                140
                          135
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145 150 155 160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
165 170 175
                 165
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
                                  185
            180
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
                                                220
                         215
  210
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245 250 255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
265 270
                                  265
             260
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
275 280 285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290 295 300
   290
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305 310 315 320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
370 380
                         375
  370
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385 390 395
Val Ala Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                      410
                 405
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
420 425 430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
435 440 445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450 455 460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 465 470 480
                    470
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                   505
             500
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                               520
      515
Arg Leu Ala Arg Gly His Ser Leu
                           535
    530
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<sup>&</sup>lt;210> 406

<sup>&</sup>lt;211> 312

<sup>&</sup>lt;212> PRT

<sup>&</sup>lt;213> Artificial Sequence

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<220>
<223> Mutant rep protein: rep40 74 402 495 GCG GCC GCC
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
           20
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                            40
        35
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                        55
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                                        75
                    70
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
               . 85
                                    90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                               105
           100
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                          120
                                                125
        115
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130 135 140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                                        155
                    150
145
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                   170
                165
Val Ala Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                185
           180
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                                205
                           200
        195
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                        215
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                    230
                                       235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val
                                    250
                245
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
                                                    270
           260
                               265
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                          280
                                                285
        275
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                        295
Arg Leu Ala Arg Gly His Ser Leu
305
<210> 407
<211> 621
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep78 228 462 497 GCC GCC GCC
<400> 407
Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
                                    10
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
                                                    30
                                25
            20
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
                            40
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
```

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55 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 70 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 105 110 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 140 135 130 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 145 150 155 160 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 185 180 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 205 200 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 220 Met Glu Leu Ala Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 250 245 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 265 260 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 295 300 .290 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 330 325 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 345 340 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 425 420 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Ala Lys Gln
450 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 480 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 495 Ala Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 Ala Gln Fro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 520 525 515 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 540

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 Phe
 Pro
 Cys
 Arg
 Glu
 Cys
 Glu
 Arg
 Met
 Asn
 Glu
 Asn
 Ile
 Cys
 560
 555
 555
 555
 560
 560
 560
 560
 560
 560
 560
 560
 601
 Cys
 Leu
 Glu
 Cys
 Phe
 Pro
 Val
 Ser
 Glu
 Cys
 Tyr
 Glu
 Lys
 Leu
 Cys
 Tyr
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 Glu
 Lys
 Leu
 Cys
 Tyr
 Ser
 Glu
 Cys
 Tyr
 Ser
 Cys</th

<210> 408 <211> 397 <212> PRT <213> Artificial Sequence

<220>
<223> Mutant rep protein: rep52 228 462 497 GCC GCC GCC

<400> 408 Met Glu Leu Ala Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 30 25 20 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 40 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 60 55 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80 70 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 90 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 105 110 100 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 125 115 120 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 130 135 140 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 155 150 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 175 170 165 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 185 180 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 205 200 195 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 215 220 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Ala Lys Gln 235 230 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 255 245 250 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 265 Ala Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 280 285 275 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 290 295 300 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 310 315 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys

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330 325 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 345 350 340 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 355 360 365 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 370 375 380 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 390 <210> 409 <211> 536 <212> PRT <213> Artificial Sequence <223> Mutant rep protein: rep68 228 462 497 GCC GCC GCC <400> 409 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 25 20 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 40 45 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 60 50 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 70 75 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 90 85 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 110 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 140 130 135 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 160 150 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 170 165 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 190 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 205 195 200 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 215 220 210 Met Glu Leu Ala Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 235 230 235 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
260 265 270 260 265 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 280 285 275 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 310 315 305 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala

330

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Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 345 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 375 370 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 415 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 425 420 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Ala Lys Gln 450 450 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 495 Ala Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 510 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 520 515 Arg Leu Ala Arg Gly His Ser Leu 530 · 535 <210> 410 <211> 312 <212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep40 228 462 497 GCC GCC GCC

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195
                               200
                                                    205
  Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                           215
                                               220
  Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Ala Lys Gln
  Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                     250
  Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 260 265 270
  Ala Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                             280
                                                   285
  Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
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  Arg Leu Ala Arg Gly His Ser Leu
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20 25 30
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
                             40
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                          55
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 70 75 80
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                                     90
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
                                 105
                                                      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115 120 125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
                         135
                                            140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
                                         155
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
                165
                                     170
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
                                 185
                                                      190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
        195
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215
                             200
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225 230 235 240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245 250 255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
            260.
                                265
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
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Pro Ala Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
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 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
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                     310
                                         315
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325
                                      330
                                                          335
 Thr Ala Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
             340
                                 345
                                                      350
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
         355
                             360
                                                 365
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
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                         375
                                            380
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
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                    390
                                         395
                                                              400
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 410 415
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
             420
                                 425
                                                     430
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
         435
                             440
                                                 445
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
    450
                        455
                                            460
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                   470
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
                                                             480
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
            500
                                505
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                            520
                                                525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
    530
                       535
                                             540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                   550
                                        555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                565
                                    570
                                                         575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
                                585
Ile His His Fle Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
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                           600
                                               605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
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 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 20
 25

 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 35
 40

 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50
 55

 Pro Ala Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu

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Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                85
                                    90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                               105
                                                    110
           100
Thr Ala Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                                                125
                           120
        115
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                    150
                                        155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
               165
                                    170
                                                        175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                               185
           180
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195 200 205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                        215
                                            220
   210
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                                       235
                    230
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
               245
                                   250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                                285
        275
                            280
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
   290
                        295
                                            300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                    310
                                        315
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                325
                                  330
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 340 345 350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
355 360 365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                        375
                                            380
  370
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                    390
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<211> 536
<212> PRT
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Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
                            40
        35
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                        55
                                            60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
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Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 110 100 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 120 125 115 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145 150 155 160 150 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 185 190 180 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 205 195 200 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 265 260 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285 285 Pro Ala Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 315 310 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 Thr Ala Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 350 340 345 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 - 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 390 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 410 415 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
420 425 430 420 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 440 445 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 465 470 475 480 470 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 510 500 505 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 520 515 Arg Leu Ala Arg Gly His Ser Leu 530 535

<210> 414 <211> 312

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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                25
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                           40
       35
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 60
Pro Ala Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65 70 75 80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
               -85
                                    90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                                    110
                               105
           100
Thr Ala Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                                                125
                           120
        115
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                                           140
   130
                        135
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                                                            160
                    150
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                    170
                165
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
           180
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                                205
                            200
        195
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                                           220
                        215
    210
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                                        235
                    230
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                    250
                245 ·
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                                                    270
                               265
            260
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                               285
        275
                          280
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                        295
                                            300
   290
Arg Leu Ala Arg Gly His Ser Leu
305
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Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 110 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Ala Ala Gly Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 495 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ala Val Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp

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Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                       535
                                            540
    530
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                   550
                                                             560
                                        555
545
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                                   570
               565
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580 585 590
           580
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                           600
       595
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                25
           20
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
35 40
        35
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                        55
   50
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75
                    70
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                   90
               85
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                            120
                                                 125
        115
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                        135
                                            140
 130
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                   150
                                        155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                    170
                                                         175
               165
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
            180
                                185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                                 205
                            200
        195
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                                            220
                        215
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 235
                   230
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245 250 255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                                                    270
                                 265
           260
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ala Val
                            280
        275
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290 295 300
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Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                                                            320
                    310
                                       315
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                325
                                    330
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                                                   350
           340
                               345
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
       355
                          360
                                              365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                        375
                                          380
  370
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
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Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
                           40
       35
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                       55
                                           60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
                    70
                                       75
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
               85
                                   90
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
                               105
                                                   110
           100
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115 120 125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Ala Ala Gly Gly
                                           140
                        135
   130
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
                                                            160
                                       155
                   150
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
                                                       175
               165
                                   170
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
                               185
                                                   190
           180
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
                                               205
                            200
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
   210
                        215
                                           220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
                                       235
                    230
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                                       255
              245
                                  250
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                               265
            260
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                            280
                                              285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                        295
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Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala

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310
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
305
                                        . 315
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
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            340
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                       375
                                            380
    370
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                   390
                                        395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 410 415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                                     430
                                425
           420
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
       435
                            440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                    470
                                        475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
              485
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ala Val 500 505 510
           500
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
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Arg Leu Ala Arg Gly His Ser Leu
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
20 25 30
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Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                    90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
           100
                                105
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                            120
       115
                                                 125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130 135 140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                   150
                                        155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165
                                     170
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Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 260 265 270 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ala Val Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp Arg Leu Ala Arg Gly His Ser Leu 

<210> 419 <211> 621

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<213> Artificial Sequence

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<223> Mutant rep protein: rep78 86 378 GCG GCG

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265 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln

280 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu

Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 310 315 320

295

275

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285

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Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325
                                      330
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
            340
                                 345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355
                             360
                                                  365
Cys Val Asp Lys Met Val Ile Trp Trp Ala Glu Gly Lys Met Thr Ala 370 380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385 390 395 400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 410 415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
420 425 430
                                 425
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
       435
                           440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 465 470 475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                                      510
            500
                                 505
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                            520
                                                 525
      515
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 540
    530
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
545 550 555 560
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                565
                                    570
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580 590
            580
                                585
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
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                           600
                                                 605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
    610
                         615
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                                      30
                                 25
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
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Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                        55
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                    70
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
               85
                                    90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                               105
                                                    110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
       115
                          120
                                               125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                        135
                                            140
Cys Val Asp Lys Met Val Ile Trp Trp Ala Glu Gly Lys Met Thr Ala
                                      155
                    150
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                                        175
               165
                                    170
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
          180
                               185
                                                   190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                               205
                           200
       195
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 215 220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                    230
                                        235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
               245
                                   250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265. 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                               285
       275
                           280
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290 295 300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                    310
                                        315
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
               325
                                    330
                                                        335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
340 345
                              345
           340
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
                                               365
       355
                            360
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                        375
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Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                    390
                                        395
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<211> 536
<212> PRT
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<220>
<223> Mutant rep protein: rep 68 86 378 GCG GCG
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Gln				Gly 85	Ala				90					95	
			100	Lys				105					110		
		115		Ile			120					125			
	130	Trp		Ala		135					140				
145	Lys			Asp	150					155					700
				Leu 165					170					175	
			180	Asn				185					T30		
		195		Ser			200					205			
	210			Ala		215					220				
225				Gly	230					235					240
				Glu 245					250					255	
			260	Ser				265					270		
		275		Thr			280					200			
	290			Ile		295					300				
305				Pro	310					315					320
				Gly 325 Thr					330					222	
			340	Val				345					350		
		355					360					365			
	370			Met Ser		375					380				
385				Cys	390					395					400
				405 Asn					410					410	
			420	His				425					430		
		435		Arg			440					445			
	450			Phe		455					460				
165					470					475					480 Ala
				485					490					423	Val
			ຽດດ	Thr				505					2TO		
		515		Gly			520					525	-		-
wra	530		ur 9	~-y		535									

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<210> 422
<211> 312
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
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                                25
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                             40
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                         55
                                            60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                     90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                 105
                                                    110
            100
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
        115
                            120
                                                 125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130 135 140
Cys Val Asp Lys Met Val Ile Trp Trp Ala Glu Gly Lys Met Thr Ala
                    150
                                         155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
               165
                                     170
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                                    190
            180
                                 185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195
                            200
                                                 205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 225 220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                    230
                                        235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                    250
                245
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                                                    270
            260
                                 265
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                            280
                                                 285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                                             300
    290
                        295
Arg Leu Ala Arg Gly His Ser Leu
<210> 423
<211> 621
<212> PRT
<213> Artificial Sequence
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Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 1 5 10 15
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Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val Gln Phe Glu Lys Gly Ala Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val

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500 505 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 520 525 515 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 535 540 530 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 545 550 555 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 575 565 570 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580

The His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 605 600 595 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 615 610 <210> 424 <211> 536 <212> PRT <213> Artificial Sequence <220> <223> Mutant rep protein: rep68 54 86 GCC GCG Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 25 20 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 40 Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 60 50 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 Gln Phe Glu Lys Gly Ala Ser Tyr Phe His Met His Val Leu Val Glu 90 85 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 105 100 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 120 125 115 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 145 150 155 160 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 185 180 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 200 205 195 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 215

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys

Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln

265

270

230

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Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 310 315 305 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 350 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 390 395 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430 420 425 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 440 435 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 465 470 480 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 510 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 520 515 Arg Leu Ala Arg Gly His Ser Leu 530 <210> 425

<211> 621

<212> PRT

<213> Artificial Sequence

<223> Mutant rep protein: rep78 54 86 GCC GCG

<400> 425

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155 150 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 170 165 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 190 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 205 200 195 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 215 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 245 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 270 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 285 280 275 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 295 290 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 310 315 320 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
340 345 350 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 380 375 370 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 415 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
480
470
475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485
490
495 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 510 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 525 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 540 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 545 550 555 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 575 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 580 585 585 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 600 595 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 615

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<211> 536 <212> PRT <213> Artificial Sequence <223> Mutant rep protein: rep68 54 86 GCC GCG Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu . 20 25 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 40 45 Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 50 55 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 70 Gln Phe Glu Lys Gly Ala Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 110 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly 130 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 150 155 160 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 235 230 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 250 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 265 270 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 295 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser

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425
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                           440
        435
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                                             460
                         455
   450
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                   470
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485
495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
500 505 510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515 520 525
Arg Leu Ala Arg Gly His Ser Leu
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<210> 427
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<212> PRT
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Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
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           20
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
                                                  45
        35
                             40
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                                             60
                         55
    50
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                                      90
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
                                                       110
                                  105
             100
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
                              120
        115
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Ala Ala Gly Gly Gly 130 135 140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
                                          155
                    150
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
                                      170
               165
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
                                 185
             180
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
                                                 205
                              200
        195
Pro Asn Ser Asp Ala Ala Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
                                              220
  210
                         215
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 240 245 Cln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245
               245
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                                 265
            260
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                              280
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Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
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                        295
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305
                    310
                                        315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325
                                    330
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                                                    350
            340
                               345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355
                            360
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                        375
                                           380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                    390
                                        395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
               405
                                   410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
           . 420
                               425
                                                   430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                            440
        435
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                       455
    450
                                           460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                    470
                                       475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
               485
                                   490
                                                       495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                           520
        515
                                               525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
   530
                       535
                                           540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                   550
                                      555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                                                       575
               565
                                   570
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
                                                   590
                               585
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
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                                               605
       595
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
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                        615.
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<210> 428

<211> 397

<212> PRT <213> Artificial Sequence

:220>

<223> Mutant rep protein: rep52 214 495 140 GCG GCC GCC

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Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
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                                    90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100
                                105
                                                      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
        115
                            120
                                                  125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130 135 140 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145
                     150
                                         155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165 170 175
                                                          175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180 185 190
            180
                                185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                             200
                                                  205
        195
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                        215
                                              220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 235 230 240
                                        235
                    230
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245 250 255
                245
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
260 265 270
            260
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
275 280 285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                        295
                                             300
   290
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 305 310 315 320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
325 330 335
                325
                                    330
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                                345
                                                     350
            340
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
355 360 365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
 370
                         375
                                             380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                     390
<210> 429
<211> 536
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep68 214 495 140 GCG GCC GCC
Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
                                                      30
            20
                                 25
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
       35
                            40
                                                 45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                        55
                                            60
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Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val

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Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Ala Ala Gly Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 145 150 155 160 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Ala Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 250 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 415 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465 470 480 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala 485 490 495 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp Arg Leu Ala Arg Gly His Ser Leu 

<210> 430 <211> 312

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<212> PRT
 <213> Artificial Sequence
 <223> Mutant rep protein: rep40 214 495 140 GCG GCC GCC
<400> 430
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
            20
                                 25
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                             40
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                     70
                                        75
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
85 90 95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100
                                 105
                                                     110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
        115
                            120
                                                 125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130
                         135
                                             140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                    150
                                        155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165 170 175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
            180
                                 185
                                                     190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195
                             200
                                                 205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
    210
                        215
                                            220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 235
                    230
                                       235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                245
                                     250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
260 265 270
                                 265
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
        275
                            280
                                                 285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                        295
  290
                                             300
Arg Leu Ala Arg Gly His Ser Leu
305
<210> 431
<211> 621
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep78 495 511 GCC GCA
Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
```

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Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 0 . Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 190 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ala Val Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp

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```
520
        515
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                                              540
                        535
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                                                              560
                   550
                                         555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
565 570 575
                                   570
                565
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580 590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                            600
       595
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                         615
    610
<210> 432
<211> 397
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep52 495 511 GCC GCA
<400> 432
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
                                     10
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                                     30
                                 25
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
35 40 45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                                             60
                        55
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
85 90 95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                 105
            100
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                             120
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        115
                         135
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145 150 155 160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                                          175
                                     170
                165
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195 200 205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
   210
                        215
                                              220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                 245
                                    250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ala Val
                                                  285
                            280
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
```

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```
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                     310
                                        315
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                325
                                   330
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
            340
                               345
                                                 350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
        355
                            360
                                                365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
  370
                        375
                                            380 -
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385
                    390
<210> 433
<211> 536
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep68 495 511 GCC GCA
<400> 433
Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
                                    10
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
                                25
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
        35
                            40
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
   50
                        55
                                           60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
                   70
                                       75
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
85 90 95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
            100
                                105
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115 - 120 125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly
    130
                        135
                                           140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
                   150
                                      155
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
                165
                                   170
                                                        175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
           180
                                                    190
                               185
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
       195
                                                205
                            200
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
  210
                       215
                                          220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
                    230
                                      235
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245 250 255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
           260
                                                    270
                               265
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
       275
                           280
                                              285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290 295 300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
```

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310
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                                            335
                 325
                                     330
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
            340
                                  345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365
        355
                             360
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 375 380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385 390 395 400
                     390
385
Val Asp Glin Lys Cys Lys Ser Ser Ala Glin Ile Asp Pro Thr Pro Val
                                     410
                405
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
           420
                                 425
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
435
440
445
                            440
        435
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450 460
                         455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465 470 475 475
                     470
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ala Val
                                 505
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
        515
Arg Leu Ala Arg Gly His Ser Leu
```

<210> 434

<211> 312 <212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep40 495 511 GCC GCA

<400> 434 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 1 10 15 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 25 20 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 40 35 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 60 55 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 85 90 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 105 110 100 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 115 120 125 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 130 135 140 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 155 150 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg

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Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ala Val Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp Arg Leu Ala Arg Gly His Ser Leu 

<210> 435

<211> 621

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep78 495 54 GCC GCC

<400> 435 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys

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```
260
                                  265
                                                       270
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
         275
                           280
                                                 285
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                        295
                                             300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305
                    310
                                         315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
               325
                                   330
                                                          335
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
             340
                                 345
                                                      350
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                           . 360
                                                 365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385 390 395 400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
            420
                                 425
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
435 440 445
      435
                           440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
   450
                       455
                                             460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                   470
                                        475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
            500
                                505
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515 520 525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 535
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 545 550 560
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
565 570 575
                565
                                    570
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
           580
                                585
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
       595
                           600
                                                 605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
    610
<210> 436
<211> 397
<212> PRT
<213> Artificial Sequence
<220>
<223> Mutant rep protein: rep52 495 54 GCC GCC
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                25
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
35 40 45
```

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```
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                        55
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                    70
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                85
                                     90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
           100
                                105
                                                     110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                           120
       115
                                                125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130 135 140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                    150
                                        155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                                         175
                165
                                    170
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
           180
                                185
                                                    190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
       195
                           200
                                                205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 220
                        215
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                    230
                                        235
225
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                                         255
                245
                                    250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                           280
                                                285
        275
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                        295
                                            300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305
                   310
                                        315
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                325
                                    330
                                                         335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                               345
           340
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
355 360 365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                        375
                                            380
   370
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                    390
385
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<210> 437

<211> 536 <212> PRT

<213> Artificial Sequence

220>

<223> Mutant rep protein: rep68 495 54 GCC GCC

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55 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 105 110 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 145 150 155 160 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 190 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 250 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 270 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 350 Phe Tyr Gly Gys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 415 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 445 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 465 470 475 480 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala 485 490 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 505 510 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 Arg Leu Ala Arg Gly His Ser Leu

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<210> 438
 <211> 312
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Mutant rep protein: rep40 495 54 GCC GCC
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 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                 25
                                                      30
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
        35
                            40
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                        55
                                             60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 85 90 95
                                    90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100
                                105
                                                     110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
        115
                            120
                                                 125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                        135
                                             140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                    150
                                         155·
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165
                                    170
                                                         175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180 185
                                185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195 200 205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
    210
                        215
                                             220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225
                    230
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                245
                                    250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                            280
                                                 285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
   290
                        295
Arg Leu Ala Arg Gly His Ser Leu
305
<210> 439
<211> 621
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep78 197 495 GCG GCC
<400> 439
Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
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Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 70 75 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 120 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 150 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 190 Leu Thr His Val Ala Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 310 315 320 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 375 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 390 395 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 425 430 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala 485 490 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val

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500
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Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
         515
                              520
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 540

Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 545
                     550
                                         555
                                                                 560
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
565 570 575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
                                  585
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
595 600 605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                          615
<210> 440
<211> 397
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep52 197 495 GCG GCC
<400> 440
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
        35
                              40
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55 60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                     70
                                         75
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                85
                                      90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100
                                 105
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115 120 125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145 150 160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165
                                     170
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                  185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195
                              200
                                                   205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
    210
                        215
                                              220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 235 240
                                        235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                 245
                                      250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
            260
                                                       270
                                 265
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
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Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 290 295 300 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 305 310 315 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 325 330 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 340 345 350 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 355 360 365 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 370 375 380 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 390 <210> 441

<210> 441 <211> 536

<212> PRT

<213> Artificial Sequence

<220×

<223> Mutant rep protein: rep68 197 495 GCG GCC

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1 10 15 10 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 25 30 25 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 40 . Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 70 75 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 120 125 115 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 150 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 Leu Thr His Val Ala Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240 230 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 270 260 265 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu

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300
                         295
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                       315
                  310
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                                 345
            340
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                                                 365
                            360
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                       375
  370
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                    390
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 410 415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
420 425 430
                                425
           420
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450
455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                        475
465
                   470
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                            520
       515
Arg Leu Ala Arg Gly His Ser Leu
   530
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<210> 442

<211> 312

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep40 197 495 GCG GCC

<400> 442

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 10 Gin Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 20 25 30 20 25 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 45 35 40 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 55 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 85 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 100 105 110 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 120 125 115 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 135 140 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 150 155

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Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165
                                   170
                                                       175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
           180
                               185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
       195
                           200
                                               205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
   210
                       215
                                          220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                  230
                                     235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
               245
                                  250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
           260
                               265
                                                  270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
       275
                          280
                                              285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                      295
Arg Leu Ala Arg Gly His Ser Leu
305
                   310
<210> 443
<211> 621
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep78 261 20 GCC GCC
<400> 443
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Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Ala Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 25 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 40 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 75 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 110 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 150 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 190 180 185 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 220 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 230 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tŷr Ile Ser Phe Asn Ala Ala

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245
                                      250
Ser Asn Ser Arg Ala Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                                265
                                                      270
          260
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                         295
   290
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                    310
                                          315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
               325
                                     330
                                                           335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                                              380
                         375
    370
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                    390
                                          395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 410 415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                             440
        435
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455 460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                         475
                    470
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                                                  525
        515
                             520
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 545 550 550
                    550
                                         555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 565 570 575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580 585 590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
       595
                            600
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
   610
                         615
<210> 444
<211> 397
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep52 261 20 GCC GCC
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                  25
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Ser Asn Ser Arg Ala Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
        35
                            40
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                        55
                                            60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                    70
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                    90
                                                         95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100
                                105
                                                    110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
        1:15
                           120
                                                125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                        135
    130
                                            140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                    150
                                        155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165
                                    170
                                                        175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
            180
                                185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                           200
                                               205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                        215
    210
                                            220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225
                    230
                                        235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                245
                                    250
                                                        255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
            260
                                265
                                                   270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                           280
                                                285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
    290
                        295
                                            300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                    310
                                        315
                                                            320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                325
                                    330
                                                        335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 340 345
                               345
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
       355
                           360
                                                365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
  370
                        375
                                            380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
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<210> 445

<211> 536

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep68 261 20 GCC GCC

<400> 445

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 1 5 10 15 Glu His Leu Ala Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 25 30 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile

## -519-

Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 50 55 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 250 Ser Asn Ser Arg Ala Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405
410
415 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 465 470 480 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 495 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 505 510 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 520

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Arg Leu Ala Arg Gly His Ser Leu
<210> 446
<211> 312
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep40 261 20 GCC GCC
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
                                   10
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
           20
                               25
Ser Asn Ser Arg Ala Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                           40
       35
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                                           60
                       55
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                                       75
                   70
65
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                   90
                85
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                                  110
                                105
            100
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                                               125
                           120
       115
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                                           140
                       135
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                                       155
                   150
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                   170
                165
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                185
           180
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                               205
                            200
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                                           220
                       215
    210
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                                      235
                    230
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                   250
                245
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                               265
           260
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                                285
                           280
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Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
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  290
Arg Leu Ala Arg Gly His Ser Leu
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435 440 445 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val

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Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 490 485 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 510 500 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 520 515 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 540 **5**35 530 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 550 555 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 565 570 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 580 585 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 605 600 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 610

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                                 265
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                             280
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        275
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                                              300
                        295
 290
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                   310
305
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                    330
                325
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
            340
                                 345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                                                  365
        355
                             360
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                                             380
                        375
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385 390 395 400
385
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405
                                     410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
420 425 430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                                                  445
                            440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450
450
  450
                        455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465 470 475 480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                 505
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Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515 520 525
Arg Leu Ala Arg Gly His Ser Leu
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25
30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
                                                  45
                             40
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                                             60
                        55
   50
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
85 90 95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
                                105
            100
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115 120 125
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Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 135 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 150 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 190 Leu Thr His Val Ala Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 250 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 270 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 395 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 410 Ile Val Thr Ala Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435. 440 445 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 495 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 525 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 540 540 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 555 560 555 560 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 565 570 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580 585 590 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 600 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln

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610 615 620 <210> 450 <211> 397 <212> PRT <213> Artificial Sequence <223> Mutant rep protein: rep52 197 420 GCG GCC <400> 450 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 10 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 20 25 30 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 35 40 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 55 50 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 85 90 95 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 115 120 125 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 130 135 140 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 155 150 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 165 170 175 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ala Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 195 200 205 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 220 215 210 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 235 240 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 255 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 260 265 270 260 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 275 280 285 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 295 300 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 305 310 315 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 325 330 335 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 345 340 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 355

Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 370

375

380 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln

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 <213> Artificial Sequence
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Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
       35
                            40
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                        55
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
                    70
                                        75
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                85
                                    90
                                                         95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
           100
                               105
                                                    110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
       115
                            120
                                                125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
                                        155
                    150
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
                                    170
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
180 185 190
Leu Thr His Val Ala Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
       195
                            200
                                                205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
210 215 220
                                            220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225
                    230
                                       235
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                    250
               245
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
260 265 270
           260
                                265
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                            280
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
    290
                        295
                                            300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                   310
                                       315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
       355
                            360
                                                365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
370 380
                        375
                                           380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385 390 395 400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                    410
                                                         415
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Ile Val Thr Ala Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 445 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 490 495 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 505 510 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 Arg Leu Ala Arg Gly His Ser Leu 530

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<213> Artificial Sequence

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<223> Mutant rep protein: rep40 197 420 GCG GCC

<400> 452

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 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
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                        295
                                              300
 Arg Leu Ala Arg Gly His Ser Leu
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Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
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                                 25
                                                      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
        35
                             40
Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                       55
                                            60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
85 90
                85
                                    90
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
100 105 110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
        115
                             120
                                                 125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140
                                           140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 145 150 155 160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
165 170 175
                                                          175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
            180
                                                     190
                                185
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
        195
                            200
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
  210
                      215
                                            220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240
                     230
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245 250 255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
           260
                                                     270
                                265
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                           280
                                               285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                    310
                                         315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330
                                    330
Thr Ala Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
            340
                                345
                                                    350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365
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Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370
                                            380
                         375
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                    390
                                        395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                425
            420
                                                    430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                           440
                                                445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450 460
    450
                       455
                                           460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                    470
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
485 490 495
                                    490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
            500
                               505
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515 520 525
                           520·
                                                525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                    550
                                        555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                565
                                   570
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
           580
                               585
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                           600
                                                605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
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                        615
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150
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165
                                     170
                                                          175
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
            180
                                185
                                                     190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195
                           200
                                                205
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
    210
                        215
                                             220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                     230
                                        235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                245
                                    250
                                                         255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
            260
                                265
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 275 280 285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
    290
                         295
                                             300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 305 310 315 320
                                        315
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                325
                                   330
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
            340
                               345
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
355 360 365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                         375 .
                                             380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
<210> 455
<211> 536
<212> PRT
<213> Artificial Sequence
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<400> 455
Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
          20
                                25
                                                    30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
       35
                            40
                                                 45
Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
50 60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                                  90
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
           100
                               105
                                                   110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115 120 125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
                    150
                                        155
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Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
               165
                                   170
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
            180
                                185
                                                    190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
        195
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
    210
                        215
                                           220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
                   230
                                      235
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
             245
                                    250
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
            260
                                265
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
        275
                            280
                                              285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
   290
                       295
                                            300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                  310
                                       315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335
Thr Ala Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
            340
                                345
                                                    350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355
                            360
                                               365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370
                       375
                                           380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                  390
                                      395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
            420
                                425
                                                    430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435
                           440
                                               445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
    450
                       455
                                           460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                 470
                                      475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
           500
                               505
                                                   510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                          520
       515
Arg Leu Ala Arg Gly His Ser Leu
   530
<210> 456
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<211> 312

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep40 54 338 495 GCC GCC GCC

<400> 456

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 1 5 10 15 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Fhe Asn Ala Ala

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20
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
         35
                              40
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55
                         55
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65 70 75 80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
85 90 95
                                       90
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
             100
                                  105
                                                       110
 Thr Ala Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
        115
                            120
                                                  125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130 135 140
                                              140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145 150 160
                                          155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                 165
                                      170
                                                           175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
             180
                                  185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
       195
                             200
                                                 205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 215 220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 235 240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                 245
                                      250
                                                          255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
260 265 270
                                 265
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
       275
                            280
                                                 285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
 290
                         295
                                               300
Arg Leu Ala Arg Gly His Ser Leu
305
<210> 457
<211> 621
<212> PRT
<213> Artificial Sequence
<220>
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<400> 457
Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
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Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
20 25 30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
35 40 45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                        55
                                             60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80
                                          75
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                85
                                    90
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
100 105 110
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Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 120 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 145 150 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 Leu Thr His Val Ala Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Tle Thr Ser Glu Lys 225 230 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 330 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 350 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Ala Ile Asp Gly Asn Ser 420 425 430 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 440 435 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 465 470 480 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 510 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 525 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 535 . 540 535 540 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 550 555 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 565 570 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 585 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp

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600
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
    610
                         615
<210> 458
<211> 397
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep52 197 427 GCG GCG
<400> 458
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                                      10
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
           20
                                  25
                                                     30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                            40
        35
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
85 90 95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
           100
                                 105
                                                     110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115 120 125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130
                         135
                                              140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                   150
                                        155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
               165
                                                          175
                                    170
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180 185 190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Ala Ile Asp Gly Asn Ser
        195
                             200
                                                  205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
 - 210
                         215
                                              220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 235 240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 255
                245
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
        275
                            280
                                                  285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                        295
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 305 310 315 320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                325
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
            340
                                 345
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
        355
                            360
                                                  365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 370 375 380
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Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
 385
                     390
 <210> 459
 <211> 536
 <212> PRT
 <213> Artificial Sequence
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Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
            20
                                 25
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
        35
                             40
                                                 45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                        55
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80
                                        75
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                85
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
            100
                                 105
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115 120 125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly
                       135
                                            140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
                    150
                                        155
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
                165
                                    170
                                                         175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
            180
                                185
                                                    190
Leu Thr His Val Ala Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
       195
                            200
                                                 205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
                       215
                                            220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245
                                    250
                                                        255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
            260
                                265
                                                    270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
        275
                            280
                                                285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
    290
                       295
                                            300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                    310
                                        315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
325 330 335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
            340
                                345
                                                    350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                          360
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                        375
                                            380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
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390
                                            395
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 410
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Ala Ile Asp Gly Asn Ser
            420
                                  425
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435
                            440
                                                   445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 465 470 475 480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
500 510
                                 505
                                                        510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515 520 525
      515
Arg Leu Ala Arg Gly His Ser Leu
    530
<210> 460
<211> 312
<212> PRT
<213> Artificial Sequence
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<400> 460
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                                       10
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
            20
                                  25
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
       35
                             40
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55 60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80
                   70
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                 85
                                      90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100 105 110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115 120 125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130 135 140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                     150
                                          155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165 170 175
                165
                                     170
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180 185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Ala Ile Asp Gly Asn Ser 195 200 205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 215 220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                    230
                                         235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
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250

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<210> 461

<211> 621

<212> PRT-

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep78 54 228 370 387 GCC GCC
GCC GCG

<400> 461 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 1 10 15 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 25 30 25 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 40. Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 60 50 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 75 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 110 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 140 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 145 150 150 160 150 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 190 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 220 Met Glu Leu Ala Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 270 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 310 320 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330

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Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
            340
                               345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
       355
                           360
                                               365
Cys Ala Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
   370
                       375
Lys Val Ala Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                   390
                                       395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
              405
                                  410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
         420
                              425
                                                  430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                           440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                       455
   450
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                       475
                  470
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
             485
                                  490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
           500
                               505
                                                  510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                           520
       515
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
   530
                       535
                                           540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                   550
                                      555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
565 570 575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
                                                  590
           580
                               585
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                           600
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                       615
```

<210> 462

<211> 397

<212> PRT

<213> Artificial Sequence

:220>

<223> Mutant rep protein: rep52 54 228 370 387 GCC GCC GCC GCC

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Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
       115
                            120
                                                  125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                         135
Cys Ala Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                     150
                                          155
                                                                160
145
Lys Val Ala Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                 165
                                      170
                                                           175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                 185
            180
                                                     190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195 200 205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                         215
                                               220
    210
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225
                     230
                                          235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                 245
                                                           255
                                     250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
275 280 285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                         295
    290
                                               300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 305 310 315 320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
325 330 335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 340 345 350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
355 360 365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 370 375 380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                     390
<210> 463
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<211> 536

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep68 54 228 370 387 GCC GCC GCC GCC GCC

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp

1 5 10 15

Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
20 25 30

Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
35 40 45

Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu

Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
50 55 60

Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65 70 75 80

Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu

85 90 95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
100 105 110

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```
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
                            120
       115
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly
                        135
                                            140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
                   150
                                      155
145
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
165 170 175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
                                185
            180
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
195 200 205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
                       215
                                            220
Met Glu Leu Ala Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225 230 235 240
225
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                                        255
                245
                                    250
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
           260
                                265
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
        275
                           280
                                                285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                       295
                                           300
   290
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                   310
                                       315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
           340
                                345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                                                365
                            360
Cys Ala Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                       375
                                           380
   370
Lys Val Ala Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                    390
                                       395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                                    430
           420
                                425
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435
                           440
                                                445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450 460
                       455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                    470
                                       475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
               485
                                    490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
           500
                               505
                                                    510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515
                           520
Arg Leu Ala Arg Gly His Ser Leu
   530
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<sup>&</sup>lt;210> 464

<sup>&</sup>lt;211> 312

<sup>&</sup>lt;212> PRT <213> Artificial Sequence

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<223> Mutant rep protein: rep40 54 228 370 387 GCC GCC GCC GCC

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<400> 464
Met Glu Leu Ala Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
                                    10
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
           20
                                                    30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
       35
                            40
                                                45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                       55
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                    70
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                85
                                                        95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
           100
                                105
                                                    110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
       115
                           120
                                                125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130 135 140
Cys Ala Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                    150
                                        155
Lys Val Ala Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
               165
                                    170
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                185
                                                   190
           180
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
       195
                           200
                                                205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
   210
                       215
                                            220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                   230
                                        235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
               245
                                    250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
           260
                               265
                                                    270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
       275
                          280
                                               285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
 290
                       295
                                            300
Arg Leu Ala Arg Gly His Ser Leu
```

<210> 465

<211> 621

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep78 221 289 GCA GCC

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310
310
320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 335 325 330 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 350 340 345 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 - 360 365 360 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 415 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 495 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 510 500 505 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 520 525 515 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu

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<210> 466-<211> 397

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep52 221 289 GCA GCC

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325
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
            340
                                 345
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
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       355
                                                  365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
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                         375
                                            380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
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<211> 536
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<213> Artificial Sequence
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20 25 30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
                             40
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
50 60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 70 75 80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                85
                                     90
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
            100
                                 105
                                                       110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115 120 125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145 150 155 160
                                          155
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
                                      170
                165
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
            180
                                 185
                                                      190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
       195
                             200
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ala Ala Arg Tyr 210 215 · 220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245
                                     250
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285
Ala Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290 295 300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325
                    310
                                         315
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Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro-345 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 390 395 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 410 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 440 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 495 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 520 Arg Leu Ala Arg Gly His Ser Leu 530 535

<210> 468

<211> 312

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep40 221 289 GCA GCC

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260

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200 205 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 215 220 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 230 235 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 260 265 270 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 275 280 285 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 295 290 Arg Leu Ala Arg Gly His Ser Leu <210> 469 <211> 621 <212> PRT <213> Artificial Sequence <223> Mutant rep protein: rep78 54 163 GCC GCT Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 40 45 Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 70 75 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 95 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 140 135 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 145 150 155 160 Thr Gln Ala Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 190 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 235 Gin Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys

265 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 280

270

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Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                        295
    290
                                            300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                    310
                                        315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335
                                  330 ^
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                               345
                                                    350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                            360
        355
                                                365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370
                        375
                                           380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                       395
                   390
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
            420
                               425
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                            440
                                                445
       435
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
    450
                       455
                                           460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                  470
                                       475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
           500
                               505
                                                    510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
       515
                           520
                                               525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                       535
                                           540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                   550
                                      555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                565
                                   570
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
           580
                               585
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
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                           600
                                               605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
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                        615
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<211> 536

<212> PRT <213> Artificial Sequence

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70 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 150 155 Thr Gln Ala Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 185 180 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 205 195 200 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 215 220 210 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 270 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 285 275 280 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 310 315 320 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 380 375 370 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400 390 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 415 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 465 470 475 480 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 495 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 505 500 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 525 520 Arg Leu Ala Arg Gly His Ser Leu 530

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<211> 621 <212> PRT <213> Artificial Sequence <220> <223> Mutant rep protein: rep78 341 407 420 GCC GCC GCC <400> 471 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 25 30 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 40 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 70 75 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 110 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 150 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 , 190 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 230 235 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 270 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 300 290 295 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 335 330 Thr Thr Gly Lys Ala Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 390 400 395 Val Asp Gln Lys Cys Lys Ala Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 Ile Val Thr Ala Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser

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Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
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                            440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                  470
                                        475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
              485
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
           500
                               505
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                            520
       515
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
530 535 540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                                        555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                                  570
                565
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580 585 590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
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Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
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Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
       35
                           40
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55 60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
85 90 95
               85
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100 105 110
            100
                                105
Thr Thr Gly Lys Ala Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                            120
                                                125
       115
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                        135
                                            140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                  150
                                      155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165
                                   170
Val Asp Gln Lys Cys Lys Ala Ser Ala Gln Ile Asp Pro Thr Pro Val
                                                    190
            180
                                185
Ile Val Thr Ala Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                            200
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Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 215 220 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 230 235 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 255 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 265 260 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 280 285 275 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 295 300 290 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 305 310 315 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 330 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 340 345 350 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 360 365 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 380 370 375 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 390

<210> 473

<211> 536

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep68 341 407 420 GCC GCC GCC

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215
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245 250 255
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
            260
                                 265
                                                      270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
        275
                           280
                                                285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                        295
    290
                                              300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                    310
                                          315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                 325
                                      330
                                                           335
Thr Thr Gly Lys Ala Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
            340
                                 345
                                                      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
   370
                        375
                                             380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385 390 400
Val Asp Gln Lys Cys Lys Ala Ser Ala Gln Ile Asp Pro Thr Pro Val
                 405
                                     410
                                                          415
Ile Val Thr Ala Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
            420
                                425
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455 460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                   470
                                         475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                485
                                     490
                                                          495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
            500
                                505
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515 - 520 525
     515 -
Arg Leu Ala Arg Gly His Ser Leu
   530
                         535
<210> 474
<211> 312
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
35 40 45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55 60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65 70 75 80
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Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                85
                                    90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100
                                105
Thr Thr Gly Lys Ala Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                                               125
                           120
        115
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                    150
                                        155
                                                            160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
               165
                                    170
                                                        175
Val Asp Gln Lys Cys Lys Ala Ser Ala Gln Ile Asp Pro Thr Pro Val
           180
                                185
                                                   190
Ile Val Thr Ala Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195
                            200
                                                205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
   210
                        215
                                            220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                    230
                                       235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                245
                                   250
                                                        255 -
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                                                   270
                               265
           260
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
        275
                            280
                                                285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                        295
   290
Arg Leu Ala Arg Gly His Ser Leu
305
                    310
<210> 475
<211> 621
<212> PRT
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<213> Artificial Sequence

<223> Mutant -rep protein: rep78 54 228 GCC GCC

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu

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170
                 165
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
                                185
                                                      190
           180
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
195 200 205
                                                 205
       195
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 220
                         215
   210
Met Glu Leu Ala Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225 230 235 240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                                           255
               245
                                     250
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                                265
                                                      270
            260
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
        275
                            280
                                                 285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
  290
                         295
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                     310
                                          315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                         375
                                             380
    370
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                         395
                    390
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 410
                                    410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                             440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                    470
                                         475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
500 505 510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                             520
                                                  525
        515
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                                              540
                        535
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                    550
                                         555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
565 570 575
                565
                                   570
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580 585 590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
595 600 605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                         615
   610
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<210> 476

<sup>&</sup>lt;211> 397 <212> PRT

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<213> Artificial Sequence
<223> Mutant rep protein: rep52 54 228 GCC GCC
<400> 476
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
            20
                                25
                                                    30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
        35
                            40
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
    50
                        55
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                    70
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
               85
                                   90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                105
                                                    110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                            120
        115
                                                125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130
                        135
                                            140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                   150
                                       155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
               165
                                    170
                                                        175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
            180
                                185
                                                   190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195
                            200
                                                205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
    210
                        215
                                            220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225
                    230
                                      235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
               245
                                                       255
                                   250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                                265
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
        275
                           280
                                               285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
    290
                        295
                                           300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                   310
                                      315
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
               325
                                   330
                                                       335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
            340
                               345
                                                   350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
       355
                           360
                                               365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                        375
                                          380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385
                   390
<210> 477
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<sup>&</sup>lt;211> 536

<sup>&</sup>lt;212> PRT

<sup>&</sup>lt;213> Artificial Sequence

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<220> <223> Mutant rep protein: rep68 54 228 GCC GCC

<400> 477 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Ala Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val. Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln

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```
455
     450
                                             460
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                   470
                                       475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
                                    490
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
            500
                                505
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 525
 Arg Leu Ala Arg Gly His Ser Leu
 <210> 478
 <211> 312
 <212> PRT
 <213> Artificial Sequence
. <223> Mutant rep protein: rep40 54 228 GCC GCC
 <400> 478
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                25
            20
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                            40
        35
                                                45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55 60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65 70 75 80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                85
                                    90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100
                                105
                                                    110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
        115
                            120
                                                125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                        135
                                            140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                   150
                                       155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165
                                    170
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180 185 190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195
                            200
                                                205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 215 220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225
                   230
                                       235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245 250 255
                245
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                                                   270
           260
                                265
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                                285
                           280
        275
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                        295
  290
                                            300
Arg Leu Ala Arg Gly His Ser Leu
                    310
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<210> 479
<211> 621
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep78 96 125 511 GCA GCG GCA
<400> 479
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Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
20 25 30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
        35
                            40
                                                 45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                        55
   50
                                            60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
                    70
                                        75
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Ala
                85
                                     90
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
            100
                                 105
                                                    110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Ala Pro Thr Leu
115 120 125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
                    150
                                        155
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
165 170 175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
            180
                                185
                                                    190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
      195
                           200
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
                    230
                                        235
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245 250 255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
           260
                                265
                                                    270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
       275
                           280
                                               285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
   290
                        295
                                            300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305
                    310
                                        315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325
                                    330
                                                         335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
           340
                               345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                        375
                                            380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                        395
                   390
385
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405
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Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 445 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 460 455 450 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 475 470 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ala Val . 500 505 510 505 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 520 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 535 540 530 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 545 550 555 560 550 555 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 565 570 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 580 585 590 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 595 600 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 615 610

<210> 480 <211> 397

<212> PRT <213> Artificial Sequence

<220>

<223> Mutant rep protein: rep52 96 125 511 GCA GCG GCA

<400> 480 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 20 25 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 55 60 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 70 75 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 90 85 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 100 105 110 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 120 115 125 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 130 135 140 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 155 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 165 170 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 185 190 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser

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200 195 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 215 220 210 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 235 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 270 265 260 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ala Val 280 285 275 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 290 295 300 - 290 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 310 315 320 305 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 330 325 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 350 345 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 355 360 365 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 370 380 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 385 <210> 481 <211> 536 <212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep68 96 125 511 GCA GCG GCA

<400> 481 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 10 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 45 40 35 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 50 55 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Ala 85 -90 . Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 110 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Ala Pro Thr Leu 115 120 125 115 120 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 145 150 155 160 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 175 170 165 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 190 185 180 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 200 205

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Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
    210
                        215
                                            220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
                    230
                                      235
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                   250
               245
                                                       255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
            260
                               265
                                                   270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                            280
                                               285
        275
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
    290 -
                       295
                                           300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                       315
                   310
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
            340
                                345
                                                   350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
       355
                            360
                                               365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                       375
                                          380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                   390
                                       395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
               405
                                   410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
           420
                                425
                                                   430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
       435
                           440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
   450
                      455
                                          460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                   470
                                       475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
               485
                                   490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ala Val
           500
                               505
                                                   510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515
                           520
Arg Leu Ala Arg Gly His Ser Leu
   530
                       535
<210> 482
<211> 312
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep40 96 125 511 GCA GCG GCA
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Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
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                                                         95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                                     110
            100
                                105
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
       115
                            120
                                                 125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 130 135 140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                    150
                                         155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                     170
                165
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                185
                                                   190
           180
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195
                           200
                                                205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                        215
                                             220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                                        235
225
                    230
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245 250 255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ala Val
       275
                          280
                                                285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                       295
 290
                                             300
Arg Leu Ala Arg Gly His Ser Leu
<210> 483
<211> 621
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep78 54 163 GCC GCT
<400> 483
Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 25 30
          20
```

Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 45 35 40 Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 95 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 110 100 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 150 155

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Thr Gln Ala Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 190 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 . 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 350 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 375 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 395 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 415 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 440 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 490 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 525 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 535 540 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 550 555 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 565 570 · Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580 590 585 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 600 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 610

<210> 484 <211> 536

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<212> PRT <213> Artificial Sequence

<220>
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Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
       435
                            440
                                                 445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                       455
    450
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485
480
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                               505
           500
                                                    510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                            520
      515
Arg Leu Ala Arg Gly His Ser Leu
   530
<210> 485
<211> 621
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep78 197 420 GCG GCC
Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
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Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ala Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu

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290
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                     310
                                           315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
325 330 335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370
                          375
                                                380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                    390
                                          395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 415
Ile Val Thr Ala Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
420 425 430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                              440
                                                    445
        435
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                          455
                                               460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465 470 475 480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                                        510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515 520 525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
530 540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                                          555
                    550
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
565 570 575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580 595
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
595 600 605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
<210> 486
<211> 397 <212> PRT
<213> Artificial Sequence
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<400> 486
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
            20
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
35 40 45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                         55
                                              60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80
```

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Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                    90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                105
            100
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
        115
                            120
                                                125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                        135
                                            140
   130
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                   150
                                       155
                                                            160
145
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                    170
              165
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
           180
                                185
Ile Val Thr Ala Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195
                            200
                                                205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                        215
                                            220
   210
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                   230
                                       235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                   250
               245
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                           280
                                                285
        275
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                                            300
                       295
   290
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 305 310 315
                   310
                                       315
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
               325
                                    330
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                                345
                                                   350
           340
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
                            360
        355
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                        375
                                            380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                    390
385
<210> 487
<211> 536
<212> PRT
<213> Artificial Sequence
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:220>

<223> Mutant rep protein: rep68 197 420 GCG GCC

 <400> 487

 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 1

 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 25

 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35

 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 50

 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Leu Phe Phe Val 65

 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu

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				85	_			_	90	_		_	_	95	
Thr	Thr	Gly	Val 100	Lys	Ser	Met	Val	Leu 105	Gly	Arg	Phe	Leu	Ser 110	GIn	IIe
_		115				_	120	-	_	_		125			
Pro	Asn 130	Trp	Phe	Ala	Val	Thr 135	ГЛЗ	Thr	Arg	Asn	Gly 140	Ala	Gly	Gly	Gly
Asn 145	Lys	Val	Val	Asp	Glu 150	Cys	Tyr	Ile	Pro	Asn 155	Tyr	Leu	Leu	Pro	Lys 160
			Glu	165				_	170					175	
			Leu 180					185					190		
		195	Val				200				_	205			
	210		Asp			215					220				
225			Val		230					235				_	240
	_		Gln	245	_	•			250					255	
			Arg 260				_	265			_		270		_
		275	Leu				280					285			
	290		Asp			295					300		_		_
305	_	_	Asp		310	_				315					320
			Phe	325					330					335	
			Lys 340					345					350		
		355	Сув				360					365			
	370		Lys			375					380				
385			Glu		390					395					400
•			Lys	405					410					415	
			Ala 420					425					430		
		435	Glu A~~				440					445			_
	450		Arg			455					460				
465			Asp Phe		470					475					480
				485					490					495	
-			Ala 500					505			_		510	_	_
		515	Ser	_	_	_	520	GIU	ALG	Per	115	525	+ 1 +	AL a	.asp
wrg	530	WTd	Arg	GTÅ	ms	535	neu								

<sup>&</sup>lt;210> 488 <211> 312 <212> PRT

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<213> Artificial Sequence
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                                    30
           20
                                25
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
       35
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                       55
                                            60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                                        75
65
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                   90
               85
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                                    110
           100
                                105
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                           120
       115
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
   130
                       135
                                            140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                                                            160
                                       155
                   150
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                                        175
                                    170
               165
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                                    190
                                185
           180
Ile Val Thr Ala Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                            200
                                                205
       195
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                       215
                                            220
  210
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                                                            240
                                      235
                    230
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                   250
                245
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                                                    270
                                265
           260
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                                285
                            280
       275
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                       295
                                            300
 290
Arg Leu Ala Arg Gly His Ser Leu
305
                    310
<210> 489
<211> 621
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep78 334 428 499 GCG GCT GCC
<400> 489
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Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
                                25
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
```

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	_	35	_	_			40		_	_		45		<b>5</b> 1	<b>-</b>
	Gln 50					55					60				
65	Glu				70					75					80
Gln	Phe	Glu	Lys	Gly 85	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val 95	Glu
Thr	Thr	Gly	Val 100	Lys	Ser	Met	Val	Leu 105	Gly	Arg	Phe	Leu	Ser	Gln	Ile
Arg	Glu	Lys 115		Ile	Gln	Arg	Ile 120		Arg	Gly	Ile	Glu 125	Pro	Thr	Leu
Pro	Asn 130		Phe	Ala	Val	Thr 135		Thr	Arg	Asn	Gly 140		Gly	Gly	Gly
Asn 145	Lys	Val	Val	Asp	Glu 150		Tyr	Ile	Pro	Asn 155		Leu	Leu	Pro	Lys 160
Thr	Gln	Pro	Glu	Leu 165	Gln	Trp	Ala	Trp	Thr 170	Asn	Met	Glu	Gln	Tyr 175	Leu
Ser	Ala	Cys	Leu 180		Leu	Thr	Glu	Arg 185		Arg	Leu	Val	Ala 190		His
Leu	Thr	His 195		Ser	Gln	Thr	Gln 200		Gln	Asn	Lys	Glu 205		Gln	Asn
Pro	Asn 210		Asp	Ala	Pro	Val 215		Arg	Ser	Lys	Thr 220		Ala	Arg	Tyr
Met 225	Glu	Leu	Val	Gly	Trp 230		Val	Asp	Lys	Gly 235		Thr	Ser	Glu	Lys 240
Gln	Trp	Ile	Gln	Glu 245		Gln	Ala	Ser	Tyr 250	Ile	Ser	Phe	Asn	Ala 255	Ala
Ser	Asn	Ser	Arg 260		Gln	Ile	Lys	Ala 265		Leu	Asp	Asn	Ala 270	Gly	Lys
	Met	275					280				•	285			
	Val 290					295					300				
305	Gly				310					315					320
	Lys			325					330					335	
	Thr		340					345					350		
•	Tyr	355					360					365			
-	Val 370					375					380				
385	Val				390					395					400
	Asp			405					410					415	
	Val		420					425					430		
	Thr	435					440					445			
	Leu 450					455					460				
465	Val				470					475					480
	His			485					490					495	
	Ser		500					505					510		
Ala	Gln	Pro 515	Ser	Thr	Ser	Asp	Ala 520	Glu	Ala	Ser	11e	Asn 525	TYT	АТа	Asp

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Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 535 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 550 555 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 565 570 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 580 585 590 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 595 600 605 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 610 615 <210> 490 <211> 397 <212> PRT <213> Artificial Sequence <223> Mutant rep protein: rep52 334 428 499 GCG GCT GCC Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 20 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys - 35 40 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 55 50 60 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 70 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 90 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Ala Pro Ala 100 105 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 115 -120 125 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 130 135 140 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 150 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 165 170 175 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 180 185 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ala Asp Gly Asn Ser 195 200 205 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 215 220 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 235 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 255 245 250 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 265 Pro Ser Ala Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 280 275 285 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp

295

Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu

300

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305 310 315 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 330 325 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 350 340 345. Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 360 365 355 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 380 375 370 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 390 <210> 491 <211> 536 <212> PRT <213> Artificial Sequence <223> Mutant rep protein: rep68 334 428 499 GCG GCT GCC <400> 491 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 10 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 25 30 20 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 45 40 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile .105 110 100 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 135 130 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 150 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 170 175 165 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 185 180 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 220 215 210 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 230 235 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 255 250 245 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 265 260 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 285 280 275 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 300 295 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala

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Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Ala Pro Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ala Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala Pro Ser Ala Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp Arg Leu Ala Arg Gly His Ser Leu 

<210> 492 <211> 312

<212> PRT <213> Artificial Sequence

<223> Mutant rep protein: rep40 334 428 499 GCG GCT GCC

<400> 492 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Ala Pro Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val

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```
180
                                  185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ala Asp Gly Asn Ser
        195
                            200
                                                  205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                        215
                                              220
    210
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                     230
                                          235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
            260
                                265
                                                      270
Pro Ser Ala Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                            280
        275
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290 295 300
    290
Arg Leu Ala Arg Gly His Ser Leu
<210> 493
<211> 621
<212> PRT
<213> Artificial Sequence
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<223> Mutant rep protein: rep78 197 414 GCG GCT
<400> 493
Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
                                     10
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
                                 25
                                                      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
                             40
        35
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                        55
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 75 70 80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                85
                                     90
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
100 105 110
            100
                                 105
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115 120 125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145 150 155 160
                                         155
145
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
                                                          175
                                     170
               165
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
                                                     190
            180
                                 185
Leu Thr His Val Ala Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
        195
                             200
                                                  205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
                        215
                                             220
   210
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
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250

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys

265

255

245

260

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Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
       275
                         280
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
    290
                        295
                                           300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                   310
                                       315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
               325
                                   330
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
           340
                              345
                                                   350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
355 360 365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                       375
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                   390
                                       395
385
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Ala Pro Val
               405
                                  410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
          420
                              425
                                                   430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435
                           440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                       455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                       475
                   470
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
               485
                                   490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
       515
                           520
                                               525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
   530
                       535
                                           540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                   550
                                       555
                                                           560
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
               565
                                 570
                                                       575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
                                                  590
           580
                               585
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
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Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
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<210> 494

<211> 397

<212> PRT

<213> Artificial Sequence

220>

<223> Mutant rep protein: rep52 197 414 GCG GCT

<400> 494

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Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
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                                    90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
           100
                                105
                                                    110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                            120
        115
                                                125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                        135
    130
                                            140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                    150
                                        155
                                                             160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
               165
                                    170
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Ala Pro Val
                                                   190
            180
                                185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                            200
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                    230
                                        235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
               245
                                   250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 275 280 285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
    290
                        295
                                            300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                    310 ·
                                        315
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
               325
                                   330
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
            340
                                345
                                                    350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
        355
                            360
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                        375
                                            380
   370
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385
<210> 495
<211> 536
<212> PRT
<213> Artificial Sequence
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Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
                                25
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
       35
                            40
                                                45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
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Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 125 115 120 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 135 140 130 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 150 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
165 170 175 165 170 175 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 185 190 180 Leu Thr His Val Ala Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 200 205 195 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Pro Asn Ser Asp Ala Flo 215
210
215
220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
230
235
240
240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 270 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 280 285 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 295 300 290 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 - 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 380 375 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Ala Pro Val 405 410 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 445 440 435 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 525 Arg Leu Ala Arg Gly His Ser Leu 535

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<212> PRT
<213> Artificial Sequence
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
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            20
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                             40
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                        55
                                            60
    50
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80
                    70
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                85
                                   90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                                    110
            100
                                105
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115 120
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                                            140
    130
                        135
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                                                             160
                    150
                                        155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                   170
               165
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Ala Pro Val
            180
                                185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                                205
        195
                            200
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                                            220
    210
                        215
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                    230
                                       235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                   250
                245
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
            260
                                265
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                            280
                                                285
        275
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
    290
                        295
                                            300
Arg Leu Ala Arg Gly His Ser Leu
305
                    310
<210> 497
<211> 621
<212> PRT
<213> Artificial Sequence
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Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Ala Ala Glu Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 40 Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 90 85 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 105 - 100 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Ala Leu 120 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 140 130 135 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 150 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 185 180 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 220 215 210 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 240 230 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 285 275 280 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 300 295 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 315 310 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 350 340 345 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 360 355 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 415 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 430 420 425 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 440 435 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 490 485 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val

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505
            500
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515
                            520
                                                525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                      535
                                            540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                  550
                                       555
                                                            560
545
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                                  570
               565
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
                               585
                                                   590
            580
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
       595
                           600
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
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Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Ala Ala Glu
                                                    30
                                25
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
                            40
Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                       55
                                           60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
               85
                                   90
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
                                105
           100
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Ala Leu
115 120 125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly
                       135
                                           140
  130
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145 150 155 160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
                165
                                    170
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
                               185
           180
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
                           200
                                                205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
                     215
    210
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 235 230 235
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245 250 255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                               265
           260
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Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln

280

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Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                       295
                                           300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                       315
                   310
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
              325
                                  330
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                              345
           340
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                           360
                                               365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                       375
                                           380
  370
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                  390
                                       395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                                      415
              405
                                  410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                                  430
           420
                               425
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                           440
       435
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                                          460
                       455
   450
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                      475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                                  490
               485
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                                  510
           500
                              505
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
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                           520
Arg Leu Ala Arg Gly His Ser Leu
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<210> 499

<211> 621 <212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep78 29 260 GCG GCG

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Ala Val Ala Glu 20 25 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 40 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 60 55 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 140 135 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys

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Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 250. Ser Asn Ser Ala Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 510 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 540 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 545 550 555 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 565 570 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 580 585 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 

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<211> 397
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep52 29 260 GCG GCG
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
         . 20
                                25
                                                    30
Ser Asn Ser Ala Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
       35
                            40
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
    50
                        55
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                    70
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                85
                                    90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
           100
                               105
                                                    110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                            120
                                                125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130
                        135
                                            140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                    150
                                        155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
               165
                                    170
                                                        175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180 185 190
           180
                               185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                                205
        195
                           200
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                        215
                                            220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                    230
                                        235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                245
                                   250
                                                        255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                                285
        275
                            280
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
    290
                        295
                                            300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                    310
                                        315
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
               325
                                   330
                                                        335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                                                   350
                              345
           340
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
       355
                            360
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                        375
                                            380
   370
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
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<210> 501 <211> 536

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<212> PRT <213> Artificial Sequence <223> Mutant rep protein: rep68 29 260 GCG GCG Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Ala Val Ala Glu 25. Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 40 45 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 50 55 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 105 100 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 145 150 155 160 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 190 180 185 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 215 220 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250· Ser Asn Ser Ala Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 265 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 310 315 320 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 415 405 410 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser

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Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp Arg Leu Ala Arg Gly His Ser Leu 

<210> 502 <211> 312

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep40 29 260 GCG GCG

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300
    290
                        295
Arg Leu Ala Arg Gly His Ser Leu
<210> 503
<211> 621
<212> PRT
<213> Artificial Sequence
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<400> 503
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Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
            20
                                25
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
                                                 45
                            40
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                       55
                                            60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
               85
                                    90
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
            100
                                105
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
                            120
                                                125
       115
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
                   150
                                       155
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
                165
                                    170
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
            180
                                185
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
       195
                            200
                                                205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
  210
                      215
                                            220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225 230 240
                    230
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245 250 255
                245
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                                                     270
           260
                                265
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
        275
                           280
                                               285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290 295 300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                  310
                                       315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                                                    350
            340
                               345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                           360
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                        375
```

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Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 440 435 445 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Ala Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 505 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 525 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 535 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 550 560 555 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 565 570 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 585 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 600 595 605 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 610 615

<210> 504

<211> 397 <212> PRT

<213> Artificial Sequence

<223> Mutant-rep protein: rep52 4 484 GCT GCC

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 35 40 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 70 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 85 90 95 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 100 105 110 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 115 120 125 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 135 140 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 145 150 150 160 155 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg

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165 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 180 185 190 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 195 200 205 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 215 210 220 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 235 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 255 Glu His Glu Ala Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 260 265 270 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 275 280 285 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 290 295 300 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 315 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 325 330 330 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 340 345 350 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 355 360 365 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 370 375 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln <210> 505 <211> 536 <212> PRT

<213> Artificial Sequence

<223> Mutant rep protein: rep68 4 484 GCT GCC

<400> 505

Thr Ala Gly Ala Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 25 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 40 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 50 55 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 150 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu

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```
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
            180
                                 185
                                                    190
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
        195
                             200
                                                205
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
    210
                        215
                                           220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
                    230
                                      235
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
               245
                                    250
                                                        255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
            260
                                265
                                                    270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
        275
                            280
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                       295
                                            300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                   310
                                       315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                                345
                                                   350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355
                            360
                                               365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370
                       375
                                           380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                   390
                                       395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
               405
                                   410
                                                       415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
            420
                               425
                                                   430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435
                           440
                                               445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
   450
                      455
                                           460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                470
                                      475
                                                           480
Glu His Glu Ala Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
           500
                               505
                                                   510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
       515
                           520
Arg Leu Ala Arg Gly His Ser Leu
                       535
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<210> 506

<211> 312

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep40 4 484 GCT GCC

<400> 506

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 1 5 10 15 15 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 20 25 30 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys

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Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                         55
                                              60
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                    70
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                85
                                     90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100
                                 105
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115 120 125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                        135
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145 150 155 160
                                        155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165
                                     170
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180 185 190
            180
                                 185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195
                             200
                                                  205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 225 220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 235 240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                245
                                     250
Glu His Glu Ala Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
       275
                        . 280
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                        295
Arg Leu Ala Arg Gly His Ser Leu
305
                     310
<210> 507
<211> 621
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep78 258 124 132 GCC GCC GCC
Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
                                     10
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
                                 25
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
       35
                            40
                                                 45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 50 55
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                85
                                    90
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
            100
                                105
                                                    110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ala Glu Pro Thr Leu
115 120
```

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Pro Asn Trp Ala Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 240 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Ala Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala . 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val Ala Glu Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu - 540 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 580 585 590 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln

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615
                                             620
    610
<210> 508
<211> 397
<212> PRT
<213> Artificial Sequence
<220>
<223> Mutant rep protein: rep52 258 124 132 GCC GCC GCC
<400> 508
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
1 10 15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                 25
                                                     30
Ser Ala Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 35 40 45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                        55
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                85
                                    90
                                                         95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                                                 125
                            120
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                    150
                                        155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
               165
                                    170
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180 185 190
                                185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                                 205
        195
                             200
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                                             220
                        215
    210
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                    230
                                        235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                    250
               245
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                             280
                                                 285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                        295
   290
                                             300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                                                              320
                   310
                                        315
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                325
                                    330
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
340 345 350
            340
                                345
                                                   350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
355 360 365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                        375
  370
                                            380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
```

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```
<210> 509
<211> 536
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep68 258 124 132 GCC GCC GCC
<400> 509
Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
           20
                                25
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
        35
                             40
                                                 45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                        55
                                            60
    50
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
                    70
                                        75
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                85
                                    90
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
            100
                                 105
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ala Glu Pro Thr Leu
115 120 125
Pro Asn Trp Ala Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140
    130
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
                                                             160
                    150
                                        155
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
               165
                                    170
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
180 185 190
                                                     190
            180
                                185
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
                                                 205
        195
                            200
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
    210
                        215
                                            220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                     250
               245
Ser Ala Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                                                    270
            260
                                265
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
        275
                            280
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                        295
    290
                                             300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                   310
                                         315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                                         335
                325
                                    330
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
            340
                                345
                                                     350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                                                365
        355
                            360
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                       375
                                            380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385 390 395 400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                     410
```

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```
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                               425
                                                     430
           420
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435
                            440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                       455
                                            460
  450
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                   470
                                        475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                505
                                                    510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                            520
       515
Arg Leu Ala Arg Gly His Ser Leu
```

<210> 510

<211> 312

<212> PRT

<213> Artificial Sequence

<220>
<223> Mutant rep protein: rep40 258 124 132 GCC GCC GCC

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 10 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 20 25 Ser Ala Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 35 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 55 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80 70 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 95 90 85 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 110 100 105 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 125 120 115 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 140 135 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 150 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 165 170 175 170 165 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 180 185 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 195 200 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 215 220 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 230 235 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 255 245 250 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 260 265 270 260 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val

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```
280
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
  290
                       295
Arg Leu Ala Arg Gly His Ser Leu
<210> 511
<211> 621
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep78 231 497 GCC GCC
<400> 511
Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1 5 10 15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
                                 25
           20
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
                            40
                                                45
        35
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                       55
                                            60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                                                        95
               85
                                    90
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
            100
                                105
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
                            120
       115
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly
                       135
                                            140
  130
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145 150 155 160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
                165
                                    170
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
           180
                                185
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
                                                205
       195
                            200
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
                      215
                                           220
  210
Met Glu Leu Val Gly Trp Ala Val Asp Lys Gly Ile Thr Ser Glu Lys
225 230 240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245 250 255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
            260
                                                     270
                                265
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
       275
                           280
                                               285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290 295 300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                                             320
                  310
                                        315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                                                     350
            340
                                345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
```

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```
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala.
                        375
                                           380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                       395
                    390
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
               405
                                   410
                                                      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                               425
                                                    430
           420
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
       435
                           440
                                               445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                                          460
                       455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                   470
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485
490
495
               485
                                   490
Ala Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
          500
                               505
                                                   510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                          520
                                               525
      515
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                       535
                                           540
    530
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                    550
                                       555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                                   570
               565
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
                                                   590
            580
                               585
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
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                                               605
       595
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
 610
                        615
                                            620
<210> 512
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<213> Artificial Sequence
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<220> <223> Mutant rep protein: rep52 231 497 GCC GCC

Met Glu Leu Val Gly Trp Ala Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala

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150
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                    170
               165
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                                     190
            180
                                185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                                205
        195
                            200
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
  210
                       215
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                   230
225
                                       235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 255
                                    250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
Ala Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                                285
        275
                            280
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
  290
                       295
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                                                             320
                                       315
                    310
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                325
                                    330
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
340 345 350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
       355
                            360
                                                365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                        375
                                           380
  370
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385
                    390
<210> 513
<211> 536
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Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
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Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
                                                    30
           20
                                25
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
                           40
       35
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                        55
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
                                        75
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
               85
                                    90
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
                                105
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115 120 125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly
                        135
                                            140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
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Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
               165
                                   170
                                                       175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
                                185
            180
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
        195
                           200
                                              205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
                       215
   210
Met Glu Leu Val Gly Trp Ala Val Asp Lys Gly Ile Thr Ser Glu Lys
225
                   230
                                      235
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
             245
                                   250
                                                       255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                                                   270
           260
                               265
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                           280
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
   290
                       295
                                           300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                   310
                                       315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
              325
                                  330
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                                                  350
            340
                               345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
       355
                           360
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                       375
                                           380
   370
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                   390
                                      395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
               405
                                  410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                                  430
            420 -
                             · 425
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                           440
        435
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                       455
   450
                                           460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                  470
                                      475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
               485
                                  490
Ala Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                               505
                                                   510
           500
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
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Arg Leu Ala Arg Gly His Ser Leu
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<210> 514
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<212> PRT
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<213> Artificial Sequence

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<223> Mutant rep protein: rep40 231 497 GCC GCC

<400> 514

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Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                              40
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
85 90 95
                 85
                                       90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 100 105 110
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
         115
                             120
                                                    125
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130 135 140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                      150
                                           155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                       170
                165
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180 185 190
                                  185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
         195
                              200
                                                   205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 215 220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                      230
                                          235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 255
                 245
                                      250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
Ala Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                              280
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
   290
                          295
Arg Leu Ala Arg Gly His Ser Leu
305
<210> 515
<211> 621
<212> PRT
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Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
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Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
20 25 30
                                  25
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
35 40 45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                         55
                                              60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
```

90

Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 110

85

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Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ala Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 Ser Ala Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 580 585 . 590 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp

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605
                               600
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
    610
                          615
<210> 516 <211> 397
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<213> Artificial Sequence
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
Ser Ala Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                              40
       35
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55 60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65 70 . 75 80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                 85
                                       90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                 105
                                                        110
            100
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                                                   125
                             120
        115
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                          135
                                               140
    130
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145 150 155 160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165 170 175
                                       170
                165
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                               185
            180
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195 - 200 205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 215 220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 235
                     230
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245
                 245
                                       250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
        275
                              280
                                                    285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290 295 300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 305 310 315
                     310
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 325 330 335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 340 345
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
355 360 365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
370 380
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Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
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<210> 517
<211> 536
<212> PRT
<213> Artificial Sequence
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Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
                                                    30
                                25
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
       35
                           40
                                                45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                       55
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                                    90
               85
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
                                                   110
                               105
          100
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115 120 125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
                    150
                                        155
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
                                    170
               165
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
                                                   1.90
                               185
          180
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
                           200
                                               205
       195
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ala Ala Arg Tyr
                       215
                                           220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
                                       235
                    230
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                    250
Ser Ala Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                               265
           260
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                                               285
                           280
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                                            300
                        295
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                        315
                   310
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                   330
              325
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                            360
                                                365
        355
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                        375
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
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390
                                           395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                     410
               405
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                             440
        435
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465 470 480
                   470
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 510
                                 505
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                             520
       515
Arg Leu Ala Arg Gly His Ser Leu
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<210> 518

<211> 312 <212> PRT

<213> Artificial Sequence

<223> Mutant rep protein: rep40 221 258 GCA GCC

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Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145 150 155 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 165 170 175 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 180 185 190 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 195 200 205 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 220 215 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 230 235 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250

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Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                                                    270
                                265
           260
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                                285
       275
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                        295
  290
Arg Leu Ala Arg Gly His Ser Leu
305
<210> 519
<211> 621
<212> PRT
<213> Artificial Sequence
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Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
                                     10
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
                                                     30
                                25
           20
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
                            40
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                        55
                                            60
  50
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                                   90
               85
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
                                                    110
            100
                                105
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
                                                125
                            120
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
                                            140
                       135
   130
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145 150 155 160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
                                                        175
               165
                                    170
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
                                185
            180
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
Met Glu Leu Val Gly Trp Leu Val Asp Ala Gly Ile Thr Ser Glu Lys
235 230 240
                    230
225
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255
Ser Asn Ser Arg Ser Gln Ile Ala Ala Ala Leu Asp Asn Ala Gly Lys
                                265
           260
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                                                285
                            280
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290 295 300
    290
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305 310 315
                    310
305
Thr Lys Lys Phe Gly Ala Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325
                                     330
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
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Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
       355
                            360
                                                365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                    . 375
                                           380
  370
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                                            400
                                        395
                   390
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                                       415
               405
                                    410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                                   430
                               425
           420
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                           440
                                                445
       435
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450 455 460
   450
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                                            480
                                       475
                  470
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                                    490
               485
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                                   510
           500
                               505
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                          520
      515
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
530 535 540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                   550
                                       555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                                   570
                565
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
                                                   590
           580
                               585
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                                               605
                           600
      595
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
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                                            620
   610
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                25
Ser Asn Ser Arg Ser Gln Ile Ala Ala Ala Leu Asp Asn Ala Gly Lys
                           40
      35
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                       55
                                           60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                    90
               85
Thr Lys Lys Phe Gly Ala Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
           100
                               105
                                                    110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
       115
                            120
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Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
   130
                        135
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                                        155
                    150
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                   170
                                                       175
              165
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                                  190
         · 180
                               185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                           200
                                               205
       195
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                                           220
                        215
   210
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                   230
                                       235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
               245
                                   250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                                                   270
          260
                               265
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                           280
       275
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                        295
                                           300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                   310
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
               325
                                  330
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                               345
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
355 360 365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                        375
                                           380
  370
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
<210> 521
<211> 536
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep68 234 264 326 GCG GCG GCC
<400> 521
Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
           20
                               25
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
                                               45
       35
                           40
```

Glu His Leu Pro Gly He Ser Asp Ser Phe Val Ash Hy Val Ala Glu 20 25 30

Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 40 45

Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 50 75 60

Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80

Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 95

Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 100 105 110

Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115

Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly

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135
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
                    150
                                         155
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
                                      170
                                                           175
                 165
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
                                                       190
            180
                                 185
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
      195
                             200
                                                   205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
                       215
                                             220
Met Glu Leu Val Gly Trp Leu Val Asp Ala Gly Ile Thr Ser Glu Lys 235 230 240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245 250 255
Ser Asn Ser Arg Ser Gln Ile Ala Ala Ala Leu Asp Asn Ala Gly Lys
260 265 270
            260
                                 265
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
        275
                           280
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290 295 300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                          315
                  310
305
Thr Lys Lys Phe Gly Ala Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
355 360 365
                                                   365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
   370
                        375
                                              380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385 390 395 400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                425
                                                       430
           420
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                             440
                                                  445
       435
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 460
                         455
    450
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 465 470 475 480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
500 505 510
                                505
           500
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515 520 525
Arg Leu Ala Arg Gly His Ser Leu
<210> 522
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<211> 312

<212> PRT

<213> Artificial Sequence

:220>

<223> Mutant rep protein: rep40 234 264 326 GCG GCG GCC

<400> 522

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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
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Ser Asn Ser Arg Ser Gln Ile Ala Ala Ala Leu Asp Asn Ala Gly Lys
                                                45
       35
                            40
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                       55
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                                        75
                   70
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
Thr Lys Lys Phe Gly Ala Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                105
           100
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                            120
                                                125
       115
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                        135
                                           140
   130
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                                       155
                    150
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                    170
               165
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
           180
                                185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                           200
                                                205
       195
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                    230
                                       235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                245
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
           260
                               265
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                          280
                                                285
      275
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                        295
 290
Arg Leu Ala Arg Gly His Ser Leu
305
<210> 523
<211> 621
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep78 153 398 AGC GCG
<400> 523
Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
       35
                           40
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                        55
                                            60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
                    70
                                        75
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
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														0.5	
			7	85	<b>a</b>	34 - L	T7 7	<b>+</b>	90	7	Dha	T.Au	Sar	95 Gln	Tla
Thr	Thr	GIA		ьys	ser	Met	vaı	ьец 105	GIŢ	Arg	Pne	nea	110	Gln	116
Arg	Glu	Lys 115	100 Leu	Ile	Gln	Arg	Ile 120	Tyr	Arg	Gly	Ile	Glu 125		Thr	Leu
Pro		Trp	Phe	Ala	Val	Thr 135	Lys	Thr	Arg	Asn	Gly 140		Gly	Gly	Gly
	130 Lys	Val	Val	Asp	Glu	Cys	Tyr	Ser	Pro	Asn 155		Leu	Leu	Pro	Lys 160
145 Thr	Gln	Pro	Glu	Leu	150 Gln	Trp	Ala	Trp	Thr		Met	Glu	Gln	Tyr 175	
Ser	Ala	Cys	Leu 180	165 Asn	Leu	Thr	Glu	Arg 185	170 Lys	Arg	Leu	Val	Ala 190	Gln	His
Leu	Thr	His 195	Val	Ser	Gln	Thr	Gln 200		Gln	Asn	Lys	Glu 205		Gln	Asn
Pro		Ser	Asp	Ala	Pro	Val 215		Arg	Ser	Lys	Thr 220		Ala	Arg	Tyr
	Glu	Leu	Val	Gly	Trp 230	Leu	Val	Asp	Lys	Gly 235		Thr	Ser	Glu	Lys 240
225 Gln	Trp	Ile	Gln	Glu 245	Asp	Gln	Ala	Ser	Tyr 250		Ser	Phe	Asn	Ala 255	Ala
			260	Ser				265	Ala				270	Gly	
		275					280					285		Gln	
	290					295					300			Glu	
305					310					315				Trp	320
				325					330					Pro 335	
			340					345					350	Val	
		355					360					365		Asn	
	370					375					380			Thr	
385			-		390					395				Val	400
				405					410					Pro 415	
			420					425					430	Asn	
		435					440					445		Lys	
	450					455					460			Lys	
465					470					475				Glu	400
				485					490					Pro 495	
			500					505					210	Ser	
		515					520					525		Ala	
_	530					535					540			Met	
545					550					555				Ile	560
Phe	Thr	His	Gly	Gln 565	гЛS	Asp	Cys	Leu	Glu 570	Cys	rne	Pro	val	Ser 575	GIU

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Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
                              585
          580
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
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Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
<210> 524
<211> 397
<212> PRT
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                25
            20
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
        35
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                       . 55
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                    70
                                        75
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                   90
               85
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                                    110
            100
                               105
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
        115
                            120
                                                125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                                           140
  130
                        135
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                   150
                                       155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Ala Val Arg
                                   170
               165
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                                    190
            180
                                185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                                205
       195
                            200
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
   210
                        215
                                           220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                   230
                                       235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245 250 255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                                265
                                                    270
            260
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
       275
                            280
                                                285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                       295
                                           300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                   310
                                      315
305
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                                                       335
               325
                                   330
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                                345
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Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr

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360
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
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                        375
 370
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                    390
385
<210> 525
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<212> PRT
<213> Artificial Sequence
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<400> 525
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Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
                                25
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
                            40
        35
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                                            60
   50
                        55
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
               85
                                    90 .
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
100 105 110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115 120 125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130
Asn Lys Val Val Asp Glu Cys Tyr Ser Pro Asn Tyr Leu Leu Pro Lys
145 150 155
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
               165
                                     170
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
                                                     190
                                185
           180
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
                            200
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
                       215
                                            220
   21:0
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
              245
                                     250
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                                265
           260
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285
        275
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
    290
                        295
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                   310
                                        315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                                345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                             360
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Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Ala Val Arg 390 395 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 430 420 425 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 495 485 490 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 505 510 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 520 515 Arg Leu Ala Arg Gly His Ser Leu

<210> 526 <211> 312

<212> PRT <213> Artificial Sequence

<220>
<223> Mutant rep protein: rep40 153 398 AGC GCG

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235
                    230
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                   250
                                                       255
               245
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                                                  270
                               265
           260
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                            280
                                               285
       275
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                       295
   290
Arg Leu Ala Arg Gly His Ser Leu
305
<210> 527
<211> 621
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep78 53 216 GCG GCC
<400> 527
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Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
                               25
                                                   30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
                            40
       35
Glu Gln Ala Pro Ala Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                       55
                                           60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 75 80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                                   90
               85
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
                                                   110
           100
                               105
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
                                               125
                           120
       115
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly
                                           140
  130
                       135
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145 150 155
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
               165
                                   170
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
                               185
           180
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
                           200
                                               205
       195
Pro Asn Ser Asp Ala Pro Val Ala Arg Ser Lys Thr Ser Ala Arg Tyr
                                          220
                      215
   210
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
                   230
                                      235
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                                       255
                                    250
               245
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                                                   270
                               265
           260
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                           280
                                               285
       275
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                        295
                                           300
   290
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
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Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325
                                    330
                                                       335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                                345
            340
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
       355
                            360
                                               365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                       375
                                           380
   370
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385 390 395 400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
               405
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                425
           420
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                           440
                                               445
      435
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                      455
                                           460
   450
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                   470
                                       475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                                    490
               485
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                505
            500
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                          520
                                               525
       515
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 540
   530
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                   550
                                        555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                                   570
               565
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
           580
                                585
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
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                          600
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
  610
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<210> 528 <211> 536 <212> PRT ·

<213> Artificial Sequence

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<223> Mutant rep protein: rep68 53 216 GCG GCC

 <400> 528

 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 1

 Glu His Leu Pro Gly Ile Ser Asp Ser De Val Asn Trp Val Ala Glu 25

 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35

 Glu Gln Ala Pro Ala Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 50

 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65

 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85

 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile

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105
             100
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
                             120
                                                   125
       115
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145 150 155 160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
165
                165
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
            180
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
                             200
        195
Pro Asn Ser Asp Ala Pro Val Ala Arg Ser Lys Thr Ser Ala Arg Tyr
210 215 220
                         215
    210
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                      250
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
260 265 270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 280 285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290 295 300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 310 315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                       330
                325
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                                              380
   370
                          375
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                    390
                                           395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405
                                       410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425
                                 425
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450 455 460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                          475
                    470
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 510
            500
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515 520 525
Arg Leu Ala Arg Gly His Ser Leu
    530
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<sup>&</sup>lt;211> 621

<sup>&</sup>lt;212> PRT

<sup>&</sup>lt;213> Artificial Sequence

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<220>
<223> Mutant rep protein: rep78 22 382 GCT GCG

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ala Ser Asp Ser Phe Val Asn Trp Val Ala Glu Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys . 260 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Ala Thr Ala Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln

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```
455
                                            460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                 470
                                      475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                485
                                   490
                                                       495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
           500
                               505
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                           520
                                               525
       515
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                      535
   530
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                                      555
                   550
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
565 570 575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580 585 590
                                                   590
           580
                               585
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                           600
                                               605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                        615
 610
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<210> 530

<211> 397

<212> PRT <213> Artificial Sequence

<220>
<223> Mutant rep protein: rep52 22 382 GCT GCG

<400> 530 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 20 25 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 35 40 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 55 Pro Val Glu Asp Ile Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 85 90 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 110 105 100 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 120 115 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 130 135 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Ala Thr Ala 145 150 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 170 165 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 180 185 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 195 200 205 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 215 220 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln

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Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 270 265 260 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 280 285 275 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 300 295 290 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 310 305 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 325 330 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 340 345 350 340 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 360 365 355 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 370 375 380 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 390 395 385

<210> 531

<211> 536

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep68 22 382 GCT GCG

<400> 531 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 10 Glu His Leu Pro Gly Ala Ser Asp Ser Phe Val Asn Trp Val Ala Glu Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 40 35 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 60 55 50 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 90 85 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 105 100 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 140 135 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 145 150 155 150 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 170 165 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 185 190 180 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 205 200 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 215 220 210 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 235 230 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala

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```
245
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                                                   270
           260
                               265
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                          280
                                              285
       275
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                       295
                                           300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                   310
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                                       335
                                   330
               325
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                               345
                                                   350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                           360
                                              365
       355
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Ala Thr Ala
370 380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                   390
385
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                                       415
                                   410
               405
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                              425
                                                  430
          420
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                                              445
                          440
       435
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                       455
   450
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                   470
                                       475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                                                       495
                                   490
               485
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                                   510
                              505
          500
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                          520
       515
Arg Leu Ala Arg Gly His Ser Leu
   530
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<210> 532 <211> 312

<212> PRT <213> Artificial Sequence

<220>
<223> Mutant rep protein: rep40 22 382 GCT GCG

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Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                          120
                                               125
     115
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                       135
                                           140
   130
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Ala Thr Ala
                                       155
                   150
145
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                   170
               165
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                                  190
          180
                              185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                           200
       195
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                                          220
                       215
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                   230
                                       235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                   250
               245
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                               265
                                                   270
          260
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                          280
       275
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                       295
                                           300
   290
Arg Leu Ala Arg Gly His Ser Leu
                    310
305
<210> 533
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<211> 621 <212> PRT

<213> Artificial Sequence

<223> Mutant rep protein: rep78 231 411 GCC GCA

<400> 533 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 1.0 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn

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```
200
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
                        215
                                            220
    210
Met Glu Leu Val Gly Trp Ala Val Asp Lys Gly Ile Thr Ser Glu Lys
225 230 235 240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                    250
               245
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                               265
           260
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                           280
       275
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290 295 300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                         315
                   310
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
            340
                                345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355
                             360
                                                 365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                                             380
  370
                        375
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                        395
                   390
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ala Asp Pro Thr Pro Val
                                                         415
               405
                                    410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                            440
                                                 445
       435
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450 460
  450
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                 . 470
                                        475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                485
                                    490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
500 505 510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                                             540
                        535
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                   550
                                        555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                                    570
                565
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580 585 590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                            600
       595
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 610 620
```

<sup>&</sup>lt;210> 534

<sup>&</sup>lt;211> 397 <212> PRT

<sup>&</sup>lt;213> Artificial Sequence

<sup>:220&</sup>gt;

<sup>&</sup>lt;223> Mutant rep protein: rep52 231 411 GCC GCA

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<400> 534
Met Glu Leu Val Gly Trp Ala Val Asp Lys Gly Ile Thr Ser Glu Lys
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                                    30
           20
                                25
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      35
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                   70
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
85 90 95
                                    90
               85
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
           100
                               105
                                                    110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                           120
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                        135
                                            140
   130
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                                       155
                    150
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                   170
               165
                                                        175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ala Asp Pro Thr Pro Val
            180
                               185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                           200
                                               205
       195
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                        215
                                            220
  · 210
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                    230
                                       235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                                         255
                                   250
                245
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
           260
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                                285
        275
                            280
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                        295
   290
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                                       315
                    310
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
               325
                                   330
                                                         335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 340 345 350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
355 360 365
       355
                            360
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                        375
                                            380
  370
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                    390
<210> 535
<211> 536
<212> PRT
<213> Artificial Sequence
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<223> Mutant rep protein: rep68 231 411 GCC GCA

<400> 535

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 45 40 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 105 100 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 120 125 115 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 135 140 130 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 145 150 155 160 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 170 165 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 205 200 195 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 210 220 Met Glu Leu Val Gly Trp Ala Val Asp Lys Gly Ile Thr Ser Glu Lys 230 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 250 245 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 265 260 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 280 285 275 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 295 300 290 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 345 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 360 365 355 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 380 375 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 385 390 395 400 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ala Asp Pro Thr Pro Val 410 405 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 425 430 420 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 440 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala

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485
                                    490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                       505
                                                    510
            500
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                            520
       515
Arg Leu Ala Arg Gly His Ser Leu
   530
<210> 536
<211> 312
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep40 231 411 GCC GCA
<400> 536
Met Glu Leu Val Gly Trp Ala Val Asp Lys Gly Ile Thr Ser Glu Lys
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
            20
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                                                 45
       35
                            40
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                       55
                                            60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65 70 75 80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                85
                                    90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
           100
                                105
                                                     110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
   130
                       135
                                            140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145 150 155 160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ala Asp Pro Thr Pro Val
                                185
            180
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195 200 205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                       215
                                            220
    210
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                                        235
                    230
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                245
                                    250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                                265
            260
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                           280
                                                285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                       295
                                            300
  290
Arg Leu Ala Arg Gly His Ser Leu
                    310
<210> 537 <211> 621
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<212> PRT

<400> 537

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<213> Artificial Sequence

<220> <223> Mutant rep protein: rep78 59 305 GCG GCC

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu · Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Ala Gln Arg Asp Phe Leu 55 · ` 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 115 120 125 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 220, Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Ala Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe

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```
440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                        455
                                            460
    450
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                    470
                                        475
465
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
               485
                                    490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
           500
                               505
                                                    510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
    530
                        535
                                            540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                    550
                                        555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
565 570 575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580 585 590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
       595
                            600
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                        615
   610
<210> 538
<211> 397
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep52 59 305 GCG GCC
<400> 538
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
                                    10
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
          20
                                25
```

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys · 35 -40 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 55 50 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80 Ala Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 85 90 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 105 110 100 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 120 125 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 135 140 130 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 150 155 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 165 170 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 180 185 190 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 205 195 200 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe

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```
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                    230
                                         235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                    250
                245
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                                 285
        275
                            280
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
  290
                        295
                                             300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 305 310 315 320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 325 330 335
                325
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                                345
                                                     350
            340
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
                                                365
                           360
       355
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                        375
 370
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                    390
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<210> 539

<211> 536 <212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep68 59 305 GCG GCC

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu 20 25 30 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 45 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Ala Gln Arg Asp Phe Leu 55 60 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 70 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 105 110 100 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 120 125 115 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135 140 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 155 145 150 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 170 165 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 190 180 185 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 220 215 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys

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230
                                          235
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245 250 255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
260 265 270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                            280
                                                 285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                       295
                                             300
    290
Ala Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                                               320
                    310
                                          315
305
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                                                       350
                                 345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                                             380
                        375
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385 390 395
                     390
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405
                                     410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                            440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 450 455 460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 465 470 475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
           500
                                 505
                                                      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                             520
        515
Arg Leu Ala Arg Gly His Ser Leu
<210> 540
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<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep40 59 305 GCG GCC
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 <400> 540

 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 1

 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 25

 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 35

 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50

 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Leu Glu Leu Glu Leu Gly Gln Gln Gln Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala

85

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Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                                  110
                              105
          100
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                          120
                                               125
       115
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                       135
                                           140
   130
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                                      155
                                                           160
                   150
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
             165
                                  170
                                                      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                                  190
                               185
           180
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                           200
                                              205
       195
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                       215
                                           220
 · 210
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                   230
                                      235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
               245
                                  250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
           260
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                           280
       275
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                       295
  290
Arg Leu Ala Arg Gly His Ser Leu
305
<210> 541
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<211> 621

<212> PRT

<213> Artificial Sequence

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<223> Mutant rep protein: rep78 53 231 GCG GCC

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Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His

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180
                                 185
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 195 200 205
                             200
       195
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
210 215 220
   210
Met Glu Leu Val Gly Trp Ala Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 255
                                                        255
                                    250
                245
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                                265
            260
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                                                 285
                            280
       275
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290 295 300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 305 310 315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                     330
                325
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                                 345
            340
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                       375
                                             380
  370
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                         395
                   390
385
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405
                                     410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                425
           420
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                            440
       435
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                        455
                                            460
    450
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                         475
                    470
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                485
                                     490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                           520
                                                 525
      515
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                    550
                                         555
545
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
565 570 575
                                    570
                565
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580 585 590
                                585
           580
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                           600
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                         615
                                              620
   610
<210> 542
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<sup>&</sup>lt;211> 397

<sup>&</sup>lt;212> PRT

<sup>&</sup>lt;213> Artificial Sequence

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<220>
<223> Mutant rep protein: rep52 53 231 GCG GCC
<400> 542
Met Glu Leu Val Gly Trp Ala Val Asp Lys Gly Ile Thr Ser Glu Lys
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
            20
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                             40
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                        55
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                                        75
                    70
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                85
                                    90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100
                                105
                                                    110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                            120
                                                125
        115
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                                            140
                        135
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                    150
145
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                                        175
                165
                                    170
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
            180
                                185
                                                    190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195
                            200
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                                            220
    210
                        215
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225
                    230
                                        235
                                                             240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                                        255
                245
                                    250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
           260
                                265
                                                    270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                          280
                                                285
        275
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                        295
                                            300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                    310
                                        315
305
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                                                        335
                325
                                    330
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
            340
                                345
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
                                                365
        355
                            360
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                        375
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385
                    390
<210> 543
<211> 536
<212> PRT
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<sup>&</sup>lt;213> Artificial Sequence

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<223> Mutant rep protein: rep68 53 231 GCG GCC

<400> 543 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp 10 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 40 45 45 Glu Gln Ala Pro Ala Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 55 50 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 105 100 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 120 125 115 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 140 135 130 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 150 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175 165 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 180 185 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 220 215 210 Met Glu Leu Val Gly Trp Ala Val Asp Lys Gly Ile Thr Ser Glu Lys 230 235 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 260 265 270 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 275 -285 280 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 300 295 290 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 335 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 345 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 390 395 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 415 410 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 435 440 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln

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Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                       475
                 470
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
               485 ..
                                   490
                                                       495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                               505
                                                   510
           500
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                           520
      515
Arg Leu Ala Arg Gly His Ser Leu
                       535
   530
<210> 544
<211> 312
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep40 53 231 GCG GCC
Met Glu Leu Val Gly Trp Ala Val Asp Lys Gly Ile Thr Ser Glu Lys
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
           20
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                           40
                                               45
      35
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                       55
   50
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                   70
                                       75
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                85
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                               105
                                                  110
           100
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                          120
                                               125
      115
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                       135
                                          140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                                                           160
                    150
                                       155
145
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                   170
               165
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
           180
                               185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
       195
                           200
                                               205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                                          220
                       215
   210
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                                                           240
                    230
                                       235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
               245
                                   250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                               265
          260
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                          280
                                              285
       275
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                       295
                                           300
   290
Arg Leu Ala Arg Gly His Ser Leu
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<210> 545
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<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep78 258 498 GCC GCT
<400> 545
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                                    10
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
20 25 30
                                25
            20
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
                                                45
                            40
       35
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                        55
                                            60
   50
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
                                        75
65
                    70
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                                                        95
                85
                                    90
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
100 105 110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
                                                125
                            120
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly
                        135
                                         · 140
    130
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145 150 155 160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
                                    170
                165
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
                                185
            180
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
                                                205
      195
                            200
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
                      215
                                           220
    210
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240
225
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                    250
                                                        255
                245
Ser Ala Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                                                    270
           260
                                265
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                           280
                                              285
        275
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                        295
                                            300
    290
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305
                    310
                                        315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                    330
                                                        335
                325
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                                                    350
            340
                                345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                            360
        355
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370
                        375
                                            380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                    390
                                        395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405.
                                    410
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Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 430 425 420 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 440 435 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 460 455 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 470 475 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 495 485 490 Pro Ala Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 525 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 535 530 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 550 555 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 570 565 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr 585 580 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 600 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 610

<210> 546 <211> 397

<212> PRT <213> Artificial Sequence

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<223> Mutant rep proteinrep 52 258 498 GCC GCT

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200
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 220
                         215
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                                         235
                    230
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                     250
               245
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
                                                     270
                                265
            260
Pro Ala Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                            280
                                                 285
        275
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290 295 300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305 310 315 320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                                     330
                325
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
340 350
                                                   350
                                 345
            340
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
355 360 365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                        375
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385
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Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
            20
                                 25
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
                                                 45
                             40
       35
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                        55
                                             60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 70 75
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                85
                                     90
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
            100
                                 105
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
                             120
                                                 125
       115
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 130 135
                        135
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145 150 155 160
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Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 175

Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 185

Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 200

170

165

180

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```
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
   210
                       215
                                           220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
                   230
                                      235
225
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                   250
                                                       255
               245
Ser Ala Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
           260
                               265
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                           280
                                             285
       275
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
  290
                       295
                                          300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                  310
                                       315
305
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
               325
                                   330
                                                       335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                               345
           340
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                           360
                                               365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                      375
                                          380
  370
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                                                          400
                  390
                                      395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                  410
                                                       415
               405
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                               425
                                                  430
           420
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                           440
                                               445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                      455
                                          460
   450
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                 470
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                                                       495
               485
                                   490
Pro Ala Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                               505
                                                   510
           500
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515
                          520
Arg Leu Ala Arg Gly His Ser Leu
   530
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<210> 548 <211> 312 <212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep40 258 498 GCC GCT

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Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
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               85
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
           100
                               105
                                                   110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                          120
                                               125
       115
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                       135
                                           140
   130
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                   150
                                       155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
               165
                                   170
                                                       175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                               185
           180
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                               205
                           200
       195
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                                           220
                       215
   210
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                                       235
                   230
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
               245
                                   250
                                                       255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                                                   270
           260
                                265
Pro Ala Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                               285
                           280
       275
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                       295
  290
Arg Leu Ala Arg Gly His Ser Leu
                    310
<210> 549
<211> 621
<212> PRT
<213> Artificial Sequence
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<223> Mutant rep protein: rep78 88 231 GCC GCC

<400> 549 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val Gln Phe Glu Lys Gly Glu Ser Ala Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 

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Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 185 190 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 200 205 195 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 215 220 Met Glu Leu Val Gly Trp Ala Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
260 265 270 265 260 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 285 275 280 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 295 300 290 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 325 330 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 340 345 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365 355 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 395 390 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 410 405 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 420 425 430 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 440 445 435 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450 455 460 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 475 470 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 495 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 510 · 505 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 520 525 515 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 535 540 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys 545 550 560 550 555 545 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 565 570 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580 589 585 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 600 595 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln 610

<210> 550 <211> 397

<212> PRT

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<213> Artificial Sequence
<223> Mutant rep protein: rep52 88 231 GCC GCC
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
            20
                                 25
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                             40
        35
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                                             60
                        55
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                85
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                105
                                                      110
            100
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
       115
                             120
                                                  125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130
                        135
                                             140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                    150
                                        155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165 170 175
                165
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180 185 190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                            200
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                        215 ·
    210
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 255
                                     250
                245
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
            260
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                            280
                                                  285
       275
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290 295 300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                    310 ·
                                         315
305
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                325
                                     330
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                                                     350
                                 345
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
355 360 365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp 370 380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385
<210> 551
<211> 536
<212> PRT
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<213> Artificial Sequence

<220>
<223> Mutant rep protein: rep68 88 231 GCC GCC

<400> 551 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Ala Phe His Met His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Ala Val Asp Lys Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 415 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe

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440
                                                 445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                        455
                                            460
   450
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                    470
                                        475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
               485
                                    490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
            500
                                505
                                                    510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                            520
       515
Arg Leu Ala Arg Gly His Ser Leu
                        535
<210> 552
<211> 312
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep40 88 231 GCC GCC
Met Glu Leu Val Gly Trp Ala Val Asp Lys Gly Ile Thr Ser Glu Lys
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
        35
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                        55
                                            60
   50
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 65 70 75 80
                    70
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
               85
                                    90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                                                     110
                               105
            100
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                                            140
   130
                        135
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                   150
                                       155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165 170 175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                                                    190
            180
                                185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                            200
                                                 205
       195
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                        215
                                            220
   210
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                    230
                                      235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245
250
255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                                285
                            280
       275
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                        295
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Arg Leu Ala Arg Gly His Ser Leu
<210> 553
<211> 621
<212> PRT
<213> Artificial Sequence
<223> Mutant rep protein: rep78 101 363 GCA GCC
<400> 553
Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
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Glu Hïs Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
           20
                                                    30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
                                                45
                            40
       35
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
                       55
                                            60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                85
                                   90
Thr Thr Gly Val Ala Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
                                105
                                                    110
           100
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
                                                125
                            120
       115
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
                       135
                                           140
  130
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
                    150
                                        155
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
                165
                                    170
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
                                                    190
           180
                                185
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
                                                205
                            200
       195
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
  210
                      215
                                           220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225 230 235 240
                   230
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                                    250
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                                265
           260
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                                                285
                            280
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                       295
                                           300
  290
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                        315
                    310
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325
                                    330
                                                        335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                                345
           340
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Ala Phe Pro Phe Asn Asp
                            360
                                                365
       355
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                        375
                                            380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
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```
390
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
               405
                                   410
                                                       415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                                   430
           420
                               425
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                           440
     435
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                      455
                                          460
   450
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                  470
                                       475
465
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                                   490
               485
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
           500
                              505
                                                   510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515 520 525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                       535
                                           540
   530
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                                       555
                   550
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
               565
                                   570
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
          580
                              585
                                                   590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                          600
                                               605
       595
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                       615
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<210> 554

<211> 397

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep52 101 363 GCA GCC

<400> 554 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 10 -Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 30 25 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 40 35 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 55 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 70 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 85 90 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 105 110 100 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 120 125 115 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Ala Phe Pro Phe Asn Asp 130 135 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 155 150 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg

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Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
           180
                               185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                               205
                           200
       195
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                        215
                                            220
   210
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 225 230 235 240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                245
                                    250
                                                        255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
           260
                                265
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                                285
       275
                           280
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
   290
                       295
                                            300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                                                             320
                    310
                                        315
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
               325
                                   330
                                                        335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 340 345 350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
                           360
                                                365
       355
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                        375
                                          380
  370
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
                    390
385
<210> 555
<211> 536
<212> PRT
<213> Artificial Sequence
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<223> Mutant rep protein: rep68 101 363 GCA GCC

<400> 555

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu Thr Thr Gly Val Ala Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His

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185
                                                      190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
                             200
                                                 205
        195
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
                        215
                                             220
    210
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240
225
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245
                                     250
                                                         255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
260 - 265 270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
        275
                            280
                                                 285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290 295 300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                                                              320
                     310
                                         315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325
                                     330
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
            340
                                                     350
                                 345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Ala Phe Pro Phe Asn Asp
                            360
                                                 365
        355
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 370 380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                     390
                                         395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 410 415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                                                     430
           420
                                425
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435
                            440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                        455
                                            460
    450
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                     470
                                        475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
               485
                                                         495
                                     490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
            500
                                505
                                                     510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                            520
      515
Arg Leu Ala Arg Gly His Ser Leu
   530
                        535
<210> 556
<211> 312
<212> PRT
<213> Artificial Sequence
<220>
<223> Mutant rep protein: rep40 101 363 GCA GCC
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
           20
                                 25
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Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 35 40 45

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Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 55 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 75 65 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 90 85 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 110 105 100 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 120 125 115 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Ala Phe Pro Phe Asn Asp 135 140 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 155 150 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 165 170 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 185 190 180 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser 205 200 195 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 220 215 210 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln 235 230 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 255 250 245 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 260 265 270 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 285 280 -275 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 295 300 290 Arg Leu Ala Arg Gly His Ser Leu 305 310

<210> 557 <211> 621 <212> PRT

<213> Artificial Sequence

<223> Mutant rep protein: rep78 354 132 GCC GCC

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Asn 145		Val	Val	Asp	Glu 150		Tyr	Ile	Pro	Asn 155		Leu	Leu	Pro	Lys 160
		Pro	Glu	Leu 165			Ala	Trp	Thr 170			Glu	Gln	Tyr 175	
Ser	Ala	. Cys	Leu 180	Asn	Leu	Thr	Glu	Arg 185	Lys	Arg	Leu	Val	Ala 190		His
Leu	Thr	His 195		Ser	Gln	Thr	Gln 200			Asn	Lys	Glu 205		Gln	Asn
Pro	Asn 210		Asp	Ala	Pro	Val 215		Arg	Ser	Lys	Thr 220	Ser	Ala	Arg	Tyr
Met 225		Leu	Val	Gly	Trp 230		Val	Asp	Lys	Gly 235			Ser	Glu	Lys 240
	Trp	Ile	Gln	Glu 245		Gln	Ala	Ser	Tyr 250	Ile	Ser	Phe	Asn	Ala 255	
Ser	Asn	Ser	Arg 260	Ser	Gln	Ile	Lys	Ala 265			Asp	Asn	Ala 270		Lys
Ile	Met	Ser 275		Thr	Lys	Thr	Ala 280		Asp	Tyr	Leu	Val 285		Gln	Gln
Pro	Val 290		Asp	Ile	Ser	Ser 295		Arg	Ile	Tyr	Lys 300	Ile	Leu	Glu	Leu
Asn 305	Gly	Tyr	Asp	Pro	Gln 310	Tyr	Ala	Ala	Ser	Val 315	Phe	Leu	Gly	Trp	Ala 320
Thr	Lys	Lys	Phe	Gly 325	Lys	Arg	Asn	Thr	Ile 330	Trp	Leu	Phe	Gly	Pro 335	Ala
Thr	Thr	Gly	Lys 340	Thr	Asn	Ile	Ala	Glu 345	Ala	Ile	Ala	His	Thr 350	Val	Pro
Phe	Ala	Gly 355	Cys	Val	Asn	Trp	Thr 360	Asn	Glju	Asn	Phe	Pro 365	Phe	Asn	Asp
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				Tyr 485					490					495.	
			500	Asp				505					51,0	_	
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				Gln 565					570					575	
			580	Ser				585					590		
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Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
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                            40
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55 60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
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Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
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Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100
                                105
                                                     110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115 120 125
Phe Ala Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130
                         135
                                             140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
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Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165
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                                     170
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
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Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
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                            200
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Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 215 220
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Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225 230 235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                                                          255
                245
                                     250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                                                 285
        275
                            280
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                        295
                                            300
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Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
                                         315
                    310
305
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                325
                                                          335
                                    330
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
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                               345
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
355 360 365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
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Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
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<211> 536 <212> PRT <213> Artificial Sequence <223> Mutant rep protein: rep68 354 132 GCC GCC Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu - 20 25 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile 35 40 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu 50 55 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val 65 70 75 80 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu 85 90 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile 105 100 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu 120 Pro Asn Trp Ala Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly 135 140 130 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys 150 155 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu 165 170 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His 190 180 185 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn 200 205 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr 215 220 210 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 235 240 230 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala 245 250 255 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys 270 265 260 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 280 285 275 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu 290 295 300 290 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala 310 315 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala 330 325 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro 345 350 Phe Ala Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 360 355 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala 375 380 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg 390 395 385 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val 405 410 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser

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Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
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Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
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                  470
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
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Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                            40
      35
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln 50 55 60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65 70 75 80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
85 90 95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                               105
           100
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
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                           120
Phe Ala Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
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Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
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                    150
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
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               165
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180 195
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195 200 205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe 210 220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
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                    230
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 245 250 255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
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Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
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Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
                                                 45
                             40
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
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                                             60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65 70 80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                85
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Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
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Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115 120 125
Pro Asn Trp Ala Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly
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Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
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Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
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Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
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Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
195 200 205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
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Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys 225 230 240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
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                                                         255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                                                     270
                                 265
            260
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
        275
                            280
                                                 285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
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                        295
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Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
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                                         315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325
                                     330
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
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                                 345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp 355 360 365
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Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala

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Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
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385
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Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
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                                                    430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
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Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
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                                            460
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Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
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Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
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Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
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Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
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Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu 530 540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
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Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu 565 570 575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
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Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
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Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
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Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
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                                                205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
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    210
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
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Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
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Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
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Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
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Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
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Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
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Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
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                        375
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Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
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Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
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Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
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Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
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Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
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Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
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Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
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Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
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                                                                                                    1860
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cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg caatttgaga agggagaga ctacttccac atgcacgtgc tcgtggaaac caccggggtg aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt
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                                                                                                   1140
                                                                                                   1200
                                                                                                   1260
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-656-

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                                                                                              1380
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qtcaccaagc aggaagtcaa agactttttc cggtgggcaa aggatcacgt ggttgaggtg
gagcatgaat totacgtoaa aaagggtgga gocaagaaaa gacccgcccc cagtgacgca
                                                                                              1500
                                                                                              1560
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gaagettega teaactaege agacaggtae caaaacaaat gttetegtea egtgggeatg
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                                                                                              1680
                                                                                              1740
                                                                                              1800
totgtogtca aaaaggogta toagaaactg tgctacatto atcatatoat gggaaaggtg
                                                                                              1860
ccagacgett geactgeetg egatetggte aatgtggatt tggatgaetg catetttgaa
caataaatga tttaaatcag gtatggctgc cgatggttat cttccagatt ggctcgagga
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                                                                                               180
                                                                                               240
                                                                                               300
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                                                                                               360
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gccggaggcg ggaacaaggt ggtggatgag tgctacatcc ccaattactt gctccccaaa acccagcctg agctccagtg ggcgtggact aatatggaac agtatttaag cgcctgtttg
                                                                                               480
                                                                                               540
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                                                                                               600
                                                                                               660
                                                                                               720
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cagtggatcc aggaggacca ggcctcatac atctccttca atgcggcctc caactcgcgg
tcccaaatca aggctgcctt ggacaatgcg ggaaagatta tgagcctgac taaaaaccgcc
                                                                                               780
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                                                                                               900
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                                                                                             1020
                                                                                             1080
                                                                                             1140
                                                                                              1200
                                                                                             1260
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ttgeaagace ggatgtteaa atttgaacte accegeegte tggateatga etttgggaag
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                                                                                             1440
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gatataagtg agcccaaacg ggtgcgcgag tcagttgcgc agccatcgac gtcagacgcg gaagcttcga tcaactacgc agacaggtac caaaacaaat gttctcgtca cgtgggcatg
                                                                                             1560
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                                                                                              1740
                                                                                             1800
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ccagacgett geactgeetg egatetggte aatgtggatt tggatgactg catetttgaa
                                                                                             1860
                                                                                             1920
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                                                                                             1932
cactctctct ga
<210> 566
<211> 1932
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<sup>&</sup>lt;213> Artificial Sequence

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                                                                                       120
                                                                                       180
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cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccggggtg
                                                                                       240
                                                                                       300
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt
                                                                                       360
taccgcggga tcgagccgac tttgccaaac tggttcgcgg tcacaaagac cagaaatggc gccggaggcg ggaacaaggt ggtggatgag tgctacatcc ccaattactt gctccccaaa
                                                                                       420
                                                                                       480
                                                                                       540
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                                                                                       600
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gagcagaaca aagagaatca gaatcccaat totgatgcgc cggtgatcag atcaaaaact
                                                                                       660
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                                                                                       720
                                                                                       780
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toccaaatca aggotgoott ggacaatgog ggaaagatta tgagootgac taaaaccgoo
cccgactace tggtgggcca gcagcccgtg gaggacattt ccagcaatcg gatttataaa attttggaac taaacgggta cgatccccaa tatgcggctt ccgtctttct gggatgggcc
                                                                                       900
                                                                                       960
acgaaaaagt teggcaagag gaacaccate tggetgtttg ggcetgcaac tacegggaag accaacateg eggaggeeat ageceacact gtgeeettet aegggtgegt aaactggace
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                                                                                      1080
aatgagaact tteeetteaa egactgtgte gacaagatgg tgatetggtg ggaggagggg
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gtggaccaga aatgcaagtc ctcggcccag atagacccga ctcccgtgat cgtcacctcc
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ttgcaagacc ggatgttcaa atttgaactc acccgccgtc tggatcatga ctttgggaag
                                                                                      1320
                                                                                     1380
                                                                                     1440
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gagcatgaat totacgtoaa aaagggtgga gccaagaaaa gacccgcccc cagtgacgca
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gatataagtg agcccaaacg ggtgcgcgag tcagttgcgc agccatcgac gtcagacgcg
                                                                                     1560
                                                                                     1620
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aatctgatgc tgtttccctg cagacaatgc gagagaatga atcagaattc aaatatctgc
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                                                                                     1740
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ccagacgett geactgeetg egatetggte aatgtggatt tggatgactg catetttgaa
                                                                                     1860
                                                                                      1920
caataaatga tttaaatcag gtatggctgc cgatggttat cttccagatt ggctcgagga
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tetgaeatgg atetgaatet gattgageag geaceeetga eegtggeega gaagetgeag
                                                                                       120
                                                                                       180
                                                                                       240
cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg
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caatttqaqa aqqqaqaqag ctacttccac atgcacgtgc tcgtggaaac caccggggtg
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aatotcacgg agcgtaaacg gttggtggcg cagcatotga cgcacgtgtc gcagacgcag gagcagaaca aagagaatca gaatoccaat totgatgcgc cggtgatcag atcaaaaact
                                                                                       600
                                                                                       660
                                                                                       720
tcagccaggt acatggagct ggtcgggtgg ctcgtggaca aggggattac ctcggagaag
cagtggatcc aggaggacca ggcctcatac atctccttca atgcggcctc caactcgcgg
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teccaaatea aggetgeett ggacaatgeg ggaaagatta tgageetgae taaaacegee
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## -658-

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acgaaaaagt teggeaagag gaacaceate tggetgtttg ggeetgeaac tacegggaag accaacateg eggaggeeat ageecacact gtgeeettet aegggtgegt aaactggaee
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                                                                                      1080
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aagatgaccg ccaaggtcgt ggagtcggcc aaagccattc tcggaggaag caaggtgcgc
                                                                                      1200
gtggaccaga aatgcaagte eteggeecag atagaccega etecegtgat egteacetee
                                                                                      1260
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ttgcaagacc ggatgttcaa atttgaactc acccgccgtc tggatcatga ctttgggaag
                                                                                      1320
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                                                                                      1740
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tetgtegtea aaaaggegta teagaaactg tgetacatte atcatateat gggaaaggtg ceagacgett geactgeetg egatetggte aatgtggatt tggatgactg catetttgaa
                                                                                      1800
                                                                                      1860
                                                                                      1920
caataaatga tttaaatcag gtatggctgc cgatggttat cttccagatt ggctcgagga
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cactetetet ga
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<211> 1932
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                                                                                       120
tctgacatgg atctgaatct gattgagcag gcacccctga ccgtggccga gaagctgcag
                                                                                       180
cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg
                                                                                       240
                                                                                       300
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aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt
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gccggaggcg ggaacaaggt ggtggatgag tgctacatcc ccaattactt gctcccaaa
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                                                                                       480
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gagcagaaca aagagaatca gaatcccaat tctgatgcgc cggtgatcag atcaaaaact
                                                                                       600
                                                                                       660
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cccgactace tggtgggcca gcagcccgtg gaggacattt ccagcaatcg gatttataaa attttggaac taaacgggta cgatccccaa tatgcggctt ccgtctttct gggatgggcc
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                                                                                      1020
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                                                                                      1140
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                                                                                      1260
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                                                                                      1380
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                                                                                      1680
                                                                                      1740
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tetgtegtea aaaaggegta teagaaaetg tgetacatte atcatateat gggaaaggtg
                                                                                      1860
ccagacgett gcactgeetg egatetggte aatgtggatt tggatgaetg catetttgaa
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tetgacatgg atetgaatet gattgageag geacceetga eegtggeega gaagetgeag
                                                                                   180
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taccgcggga tcgagccgac tttgccaaac tggttcgcgg tcacaaagac cagaaatggc
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gccggaggcg ggaacaaggt ggtggatgag tgctacatcc ccaattactt gctccccaaa
                                                                                   480
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                                                                                   540
                                                                                   600
                                                                                   660
gagcagaaca aagagaatca gaatcccaat totgatgogo oggtgatcag atcaaaaact
                                                                                   720
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cagiggatec aggaggacca ggeeteatae ateteettea atgeggeete caactegegg
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                                                                                   960
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                                                                                   120
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caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccggggtg
                                                                                   360
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-660-

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gagcagaaca aagagaatca gaatcccaat tetgatgege eggtgatcag atcaaaaact
                                                                                                                                                     660
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ccagacgett geactgeetg egatetggte aatgtggatt tggatgaetg catetttgaa
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                                                                                                                                                   1080
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                                                                                                                                                   1140
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1740
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                                                                                    1860
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tctgacatgg atctgaatct gattgagcag gcacccctga ccgtggccga gaagctgcag
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cgcgactttg ctacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg
                                                                                     240
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caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccggggtg
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                                                                                    1080
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                                                                                    1860
ccagacgett geactgeetg egatetggte aatgtggatt tggatgaetg catetttgaa
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<400> 573

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                                                                                                            1860
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<223> Mutant rep DNA sequence: 86 GCG
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                                                                                          1860
                                                                                          1920
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cactctctct ga
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<210> 576 <211> 1932

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caataaatga titaaatcag gtatggctgc cgatggttat cttccagatt ggctcgagga
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tctgacatgg atctgaatct gattgagcag gcacccctga ccgtggccga gaagctgcag
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caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccggggtg
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#### -665-

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tetgacatgg atetgaatet gattgageag gcaccectga cegtggccga gaagetgcag
cgcgacttte tgacggaatg gcgccgtgtg agtaaggccc cggaggccet tttetttgga
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gccggaggcg ggaacaaggt ggtggatgag tgctacatcc ccaattactt gctccccaaa acccagcctg agctccagtg ggcgtggact aatatggaac agtatttaag cgcctgtttg
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### -666-

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cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg
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                                                                           780
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1320

# -667-

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                                                                                    1260
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### -668-

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                                                                                            1860
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## <223> Mutant rep DNA sequence: 163 GCT

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cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccggggtg
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taccgcggga tcgagccgac tttgccaaac tggttcgcgg tcacaaagac cagaaatggc
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acccaggetg agetecagtg ggegtggaet aatatggaac agtatttaag egeetgtttg
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                                                                                        1500
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                                                                                        1860
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tctgacatgg atctgaatct gattgagcag gcacccctga ccgtggccga gaagctgcag
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taccgcggga tcgagccgac tttgccaaac tggttcgcgg tcacaaagac cagaaatggc
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                                                                                         660
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                                                                                         840
toccaaatoa aggotgoott ggacaatgog ggaaagatta tgagootgao taaaacogoo
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cccgactacc tggtgggcca gcagcccgtg gaggacattt ccagcaatcg gatttataaa

900

cactctctct ga

1932

### -670-

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aatgagaact ttcccttcaa cgactgtgtc gacaagatgg tgatctggtg ggaggaggga
aagatgaccg ccaaggtcgt ggagtcggcc aaagccattc tcggaggaag caaggtgcgc
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                                                                               1200
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ttgcaagacc ggatgttcaa atttgaactc accegccgtc tggatcatga ctttgggaag
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aatctgatgc tgtttccctg cagacaatgc gagagaatga atcagaattc aaatatctgc
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1740
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                                                                               1080
                                                                               1140
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gaagettega teaactacge agacaggtae caaaacaaat gttetegtea egtgggeatg
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ccagacgett geactgeetg egatetggte aatgtggatt tggatgactg catetttgaa
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caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccggggtg
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                                                                                              360
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taccgcggga tcgagccgac tttgccaaac tggttcgcgg tcacaaagac cagaaatggc
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teagecaggt acatggaget ggtegggtgg etegtggaca aggggattae eteggagaag
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                                                                                              780
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cccgactace tggtgggcca gcagcccgtg gaggacattt ccagcaatcg gatttataaa attttggaac taaacgggta cgatcccaa tatgcggctt ccgtctttct gggatgggcc
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-678-

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-681-

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1740

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1740
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#### -685-

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-687-

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<220>

## -688-

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900

### -689-

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-690-

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1620

# -691-

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-692-

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1200

### -693-

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                                                                                              960
                                                                                            1020
acgaaaaagt teggeaagag gaacaccate tggetgtttg ggeetgeaac tacegggaag
accaacatcg cggaggccat agcccacact gtgcccttct acgggtgcgt aaactggacc aatgagaact ttcccttcaa cgactgtgtc gacaagatgg tgatctggtg ggaggagggg
                                                                                            1080
                                                                                            1140
```

aagatgaccg ccaaggtcgt ggagtcggcc aaagccattc tcggaggaag caaggtgcgc

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gtggaccaga aatgcaagtc ctcggcccag atagacccga ctcccgtgat cgtcaccgct
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                                                                                             1320
aacaccaaca tgtgcgccgt gattgacggg aactcaacga ccttcgaaca ccagcagccg
ttgcaagacc ggatgttcaa atttgaactc accegeegte tggatcatga ctttgggaag
                                                                                             1380
gtcaccaage aggaagtcaa agactttttc cggtgggcaa aggatcacgt ggttgaggtg
                                                                                             1440
gagcatgaat tetaegteaa aaagggtgga gecaagaaaa gaccegeee cagtgaegea gatataagtg ageccaaacg ggtgegegag teagttgege agecategae gteagaegeg
                                                                                             1500
                                                                                             1560
gaagettega teaactaege agacaggtae caaaacaaat gttetegtea egtgggeatg
                                                                                             1620
aatctgatge tgttteeetg cagacaatge gagagaatga atcagaatte aaatatetge
                                                                                             1680
ttcactcacg gacagaaaga ctgtttagag tgctttcccg tgtcagaatc tcaacccgtt
                                                                                             1740
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                                                                                             1800
                                                                                             1860
caataaatga tttaaatcag gtatggctgc cgatggttat cttccagatt ggctcgagga
                                                                                             1920
cactctctct ga
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<211> 1932
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<220>
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                                                                                              300
                                                                                              360
                                                                                              420
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gccggaggcg ggaacaaggt ggtggatgag tgctacatcc ccaattactt gctcccaaa acccagcctg agctccagtg ggcgtggact aatatggaac agtattaag cgcctgtttg
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                                                                                              660
                                                                                              720
tcagccaggt acatggaget ggtcgggtgg ctcgtggaca aggggattac ctcggagaag
cagtggatcc aggaggacca ggcctcatac atctccttca atgcggcctc caactcgcgg
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toccaaatca aggotgoott ggacaatgog ggaaagatta tgagootgac taaaaccgoo
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cccgactacc tggtgggcca gcagcccgtg gaggacattt ccagcaatcg gatttataaa attttggaac taaacgggta cgatcccaa tatgcggctt ccgtcttct gggatgggcc
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                                                                                             1020
                                                                                             1080
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                                                                                             1200
                                                                                             1260
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                                                                                             1380
                                                                                             1440
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gatataagtg agcccaaacg ggtgcgcgag tcagttgcgc agccatcgac gtcagacgcg gaagettcga tcaactacgc agacaggtac caaaacaaat gttctcgtca cgtgggcatg
                                                                                             1560
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                                                                                             1680
                                                                                             1740
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                                                                                             1800
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ccaqacqctt qcactgcctg cgatctqqtc aatgtqqatt tggatgactg catctttgaa
                                                                                             1860
caataaatga tttaaatcag gtatggctgc cgatggttat cttccagatt ggctcgagga
                                                                                             1920
                                                                                             1932
cactetetet ga
```

<sup>&</sup>lt;210> 620

<sup>&</sup>lt;211> 1932

<sup>&</sup>lt;212> DNA

<sup>&</sup>lt;213> Artificial Sequence

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 <223> Mutant rep DNA sequence: 422 GCC
 <400> 620
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                                                                                         120
 totgacatgg atotgaatot gattgagcag gcaccoctga ccgtggccga gaagctgcag
                                                                                         180
cgcgacttte tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttetttgtg caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccggggtg
                                                                                         240
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                                                                                         360
taccgcggga tcgagccgac tttgccaaac tggttcgcgg tcacaaagac cagaaatggc gccggaggcg ggaacaaggt ggtggatgag tgctacatcc ccaattactt gctccccaaa
                                                                                         420
                                                                                         480
                                                                                         540
accoagectg agetecagtg ggegtggaet aatatggaae agtatttaag egeetgtttg
aatotcacgg agcgtaaacg gttggtggcg cagcatctga cgcacgtgtc gcagacgcag
                                                                                         600
gagcagaaca aagagaatca gaatcccaat totgatgcgc cggtgatcag atcaaaaact
                                                                                         660
tragcraggt aratggaget ggtrgggtgg recepting and aggggattar recepting cagtggater aggaggarea ggretratar attretter atgreggete caartrggg
                                                                                         720
                                                                                         780
                                                                                         840
teccaaatea aggetgeett ggacaatgeg ggaaagatta tgageetgae taaaacegee
cccgactacc tggtgggcca gcagcccgtg gaggacattt ccagcaatcg gatttataaa attttggaac taaacgggta cgatcccaa tatgcggctt ccgtctttct gggatgggcc
                                                                                         900
                                                                                         960
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                                                                                        1020
                                                                                        1080
aatgagaact ttcccttcaa cgactgtgtc gacaagatgg tgatctggtg ggaggagggg
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aagatgaccg ccaaggtcgt ggagtcggcc aaagccattc tcggaggaag caaggtgcgc
                                                                                        1200
gtggaccaga aatgcaagtc ctcggcccag atagacccga ctcccgtgat cgtcacctcc
                                                                                        1260
                                                                                        1320
aacgccaaca tgtgcgccgt gattgacggg aactcaacga ccttcgaaca ccagcagccg
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                                                                                        1440
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gagcatgaat totacgtcaa aaagggtgga gccaagaaaa gacccgcccc cagtgacgca
                                                                                        1500
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                                                                                        1560
gaagettega teaactaege agacaggtae caaaacaaat gttetegtea egtgggeatg
                                                                                        1620 .
aatctgatgc tgtttccctg cagacaatgc gagagaatga atcagaattc aaatatctgc
                                                                                       1680
                                                                                       1740
ttcactcacg gacagaaaga ctgtttagag tgctttcccg tgtcagaatc tcaacccgtt
tetgtegtea aaaaggegta teagaaactg tgetacatte ateatateat gggaaaggtg ceagacgett geactgeetg egatetggte aatgtggatt tggatgactg catetttgaa
                                                                                       1800
                                                                                       1860
                                                                                       1920
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cactctctct ga
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<211> 1932
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<223> Mutant rep DNA sequence: 424 GCG
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egegaettte tgaeggaatg gegeegtgtg agtaaggee eggaggeet titetitgtg caatttgaga aggagagag etaetteeae atgeaegtge tegtggaaae caeeggggtg aaatecatgg tittgggaeg titeetgagt eagattegeg aaaaactgat teagagaatt
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                                                                                        360
                                                                                        420
taccgcggga tcgagccgac tttgccaaac tggttcgcgg tcacaaagac cagaaatggc
gccggaggeg ggaacaaggt ggtggatgag tgctacatcc ccaattactt gctccccaaa acccagcctg agctccagtg ggcgtggact aatatggaac agtattaag cgcctgtttg
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                                                                                        600
                                                                                        660
                                                                                        720
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cagtggatec aggaggacca ggeeteatac ateteettea atgeggeete caactegegg
                                                                                        780
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teccaaatea aggetgeett ggacaatgeg ggaaagatta tgageetgae taaaacegee
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cccgactacc tggtgggcca gcagcccgtg gaggacattt ccagcaatcg gatttataaa attttggaac taaacgggta cgatccccaa tatgcggctt ccgtctttct gggatgggcc
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                                                                                            960
                                                                                           1020
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aatgagaact ttooottoaa ogactgtgto gacaagatgg tgatotggtg ggaggagggg
                                                                                           1080
                                                                                           1140
                                                                                           1200
aagatgaccg ccaaggtcgt ggagtcggcc aaagccattc tcggaggaag caaggtgcgc
gtggaccaga aatgcaagte ctcggcccag atagacccga ctcccgtgat cgtcacctcc
                                                                                           1260
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                                                                                           1380
                                                                                           1440
qtcaccaagc aggaagtcaa agactttttc cggtgggcaa aggatcacgt ggttgaggtg
gagcatgaat totacgtcaa aaagggtgga gccaagaaaa gacccgcccc cagtgacgca
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1740
                                                                                           1800
ccagacgett geactgeetg egatetggte aatgtggatt tggatgaetg catetttgaa
                                                                                           1860
caataaatga tttaaatcag gtatggctgc cgatggttat cttccagatt ggctcgagga
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cactctctct ga
<210> 622
<211> 1932
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ggcatttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat
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totgacatgg atotgaatct gattgagcag gcacccctga ccgtggccga gaagctgcag cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg
                                                                                            180
                                                                                            240
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                                                                                            420
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                                                                                            540
                                                                                            600
                                                                                            660
tcagccaggt acatggagct ggtcgggtgg ctcgtggaca aggggattac ctcggagaag
                                                                                            720
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caqtqqatcc aggaggacca ggcctcatac atctccttca atgcggcctc caactcgcgg
tcccaaatca aggctgcctt ggacaatgcg ggaaagatta tgagcctgac taaaaccgcc cccgactacc tggtgggcca gcagcccgtg gaggacattt ccagcaatcg gatttataaa attttggaac taaacgggta cgatcccaa tatgcggctt ccgtctttct gggatgggcc acgaaaaagt tcggcaagag gaacaccatc tggctgtttg ggcctgcaac taccgggaag
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                                                                                            960
                                                                                           1020
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                                                                                           1560
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                                                                                           1800
                                                                                           1860
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                                                                                           1920
```

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 <211> 1932
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 <223> Mutant rep DNA sequence:429 GCC
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tctgacatgg atctgaatct gattgagcag gcaccctga ccgtggccga gaagctgcag
                                                                                          120
                                                                                          180
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                                                                                          240
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 aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt
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                                                                                          420
                                                                                          480
 acceagectg agetecagtg ggegtggact aatatggaac agtatttaag egeetgtttg
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 gagcagaaca aagagaatca gaatcccaat tctgatgcgc cggtgatcag atcaaaaact
                                                                                          660
 tcagccaggt acatggagct ggtcgggtgg ctcgtggaca aggggattac ctcggagaag
                                                                                          720
 cagtggatcc aggaggacca ggcctcatac atctccttca atgcggcctc caactcgcgg
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                                                                                          900
                                                                                          960
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                                                                                         1080
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                                                                                         1200
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aatctgatgc tgtttccctg cagacaatgc gagagaatga atcagaattc aaatatctgc
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                                                                                        1800
ccagacgett geactgeetg egatetggte aatgtggatt tggatgaetg catetttgaa
                                                                                        1860
caataaatga tttaaatcag gtatggctgc cgatggttat cttccagatt ggctcgagga
                                                                                        1920
cactetetet ga
                                                                                        1932
<210> 624
<211> 1932
<212> DNA
<213> Artificial Sequence
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<223> Mutant rep DNA sequence: 438 GCG
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                                                                                         120
tetgacatgg atetgaatet gattgageag geacecetga eegtggeega gaagetgeag egegaettte tgaeggaatg gegeegtgtg agtaaggee eggaggeeet tttetttgtg
                                                                                         180
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caatttgaga agggagagag ctacttccac atgcacgtgc tegtggaaac caceggggtg
                                                                                         300
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt
taccgcggga tcgagccgac tttgccaaac tggttcgcgg tcacaaagac cagaaatggc
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                                                                                         420
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                                                                                    600
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cagtggatcc aggaggacca ggcctcatac atctccttca atgcggcctc caactcgcgg
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toccaaatca aggotgoott ggacaatgog ggaaagatta tgagootgac taaaaccgoo
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#### -699-

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<400> 627
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<210> 630 <211> 1932

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ttgcaagacc ggatgttcaa atttgaactc acccgccgtc tggatcatga ctttgggaag gtcaccaagc aggaagtcaa agactttttc cggtgggcaa aggatcacgt ggttgaggtg
                                                                                    1320
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                                                                                    1440
gagcatgaat totacgtcaa aaagggtgga gccaagaaaa gacccgccta cagtgacgca
                                                                                    1500
gatataagtg agcccaaacg ggtgcgcgag tcagttgcgc agccatcgac gtcagacgcg gaagcttcga tcaactacgc agacaggtac caaaacaaat gttctcgtca cgtgggcatg
                                                                                    1560
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aatotgatgo tgtttccctg cagacaatgo gagagaatga atcagaatto aaatatotgo
                                                                                    1680
1740
                                                                                    1800
ccagacgett gcactgectg egatetggte aatgtggatt tggatgaetg catetttgaa caataaatga tttaaatcag gtatggetge egatggttat ettecagatt ggetegagga
                                                                                    1860
                                                                                    1920
cactctctct ga
                                                                                    1932
<210> 637
<211> 1932
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<sup>&</sup>lt;212> DNA

<sup>&</sup>lt;213> Artificial Sequence

900

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```
<223> Mutant rep DNA sequence: 498 GCT
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                                                                                     120
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tetgacatgg atetgaatet gattgageag geacecetga eegtggeega gaagetgeag
                                                                                     180
cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg
                                                                                     240
caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccggggtg
                                                                                     300
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt taccgcggga tcgagccgac tttgccaaac tggttcgcgg tcacaaagac cagaaatggc
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geeggaggeg ggaacaaggt ggtggatgag tgetacatee ccaattaett getecceaaa
                                                                                     480
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tcccaaatca aggctgcctt ggacaatgcg ggaaagatta tgagcctgac taaaaccgcc
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cccgactacc tggtgggcca gcagcccgtg gaggacattt ccagcaatcg gatttataaa
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                                                                                     960
                                                                                    1020
accaacatog oggaggocat agoccacact gtgoccttet acgggtgogt aaactggaco
                                                                                    1080
                                                                                    1140
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aagatgaccg ccaaggtcgt ggagtcggcc aaagccattc tcggaggaag caaggtgcgc
                                                                                    1200
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gtcaccaagc aggaagtcaa agactttttc cggtgggcaa aggatcacgt ggttgaggtg
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                                                                                    1500
                                                                                    1560
                                                                                    1620
                                                                                    1680
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1740
                                                                                    1800
ccagacgett geactgeetg egatetggte aatgtggatt tggatgaetg eatetttgaa
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<211> 1932
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tetgacatgg atetgaatet gattgageag geacceetga cegtggeega gaagetgeag
                                                                                     180
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                                                                                     240
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                                                                                     360
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geeggaggeg ggaacaaggt ggtggatgag tgctacatec ccaattactt geteeccaaa
                                                                                     480
acceagectg agetecagtg ggcgtggact aatatggaac agtatttaag cgcctgtttg
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gagcagaaca aagagaatca gaatcccaat tetgatgege eggtgatcag atcaaaaact
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tcagccaggt acatggagct ggtcgggtgg ctcgtggaca aggggattac ctcggagaag
                                                                                     720
                                                                                     780
cagtggatce aggaggacca ggcctcatac atctccttca atgcggcctc caactcgcgg
teccaaatea aggetgeett ggacaatgeg ggaaagatta tgageetgae taaaacegee eeegactaee tggtgggeea geageeegtg gaggacattt ceageaateg gattataaa
                                                                                     840
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#### -708-

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                                                                                    1020
 accaacateg eggaggeeat ageceaeact gigeeettet aegggigegt aaaciggace
                                                                                    1080
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aagatgaccg ccaaggtcgt ggagtcggc aaagccattc tcggaggaag caaggtgcgc
                                                                                    1140
                                                                                    1200
 gtggaccaga aatgcaagtc ctcggcccag atagacccga ctcccgtgat cgtcacctcc
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 aacaccaaca tgtgcgccgt gattgacggg aactcaacga ccttcgaaca ccagcagccg
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 gtcaccaagc aggaagtcaa agactttttc cggtgggcaa aggatcacgt ggttgaggtg
                                                                                    1440
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1740
                                                                                    1800
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                                                                                    1860
 caataaatga tttaaatcag gtatggctgc cgatggttat cttccagatt ggctcgagga
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 cactctctct ga
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<220>
<223> Mutant rep DNA sequence: 503 GCG
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tetgacatgg atetgaatet gattgagcag geaceeetga eegtggeega gaagetgeag
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cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccggggtg
                                                                                     240
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                                                                                     360
                                                                                     420
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                                                                                     480
                                                                                     540
                                                                                     600
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                                                                                     660
teagccaggt acatggaget ggtegggtgg etegtggaca aggggattae eteggagaag
                                                                                     720
cagtggatcc aggaggacca ggcctcatac atctccttca atgcggcctc caactcgcgg
                                                                                     780
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                                                                                     840
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                                                                                   1140
                                                                                   1200
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ttgcaagacc ggatgttcaa atttgaactc acccgccgtc tggatcatga ctttgggaag
                                                                                   1320
                                                                                   1380
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                                                                                   1500
gatatagogg agoccaaacg ggtgogogag toagttgogo agocatogac gtoagaogog
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                                                                                   1740
1800
ccagacgett geactgeetg egatetggte aatgtggatt tggatgaetg catettigaa
                                                                                   1860
caataaatga tttaaatcag gtatggctgc cgatggttat cttccagatt ggctcgagga
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cactctctct ga
                                                                                   1932
```

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 <211> 1932
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 <213> Artificial Sequence
 <223> Mutant rep DNA sequence: 510 GCA
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                                                                                      120
 totgacatgg atotgaatot gattgagoag goaccootga cogtggooga gaagotgoag
                                                                                      180
 cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccggggtg
                                                                                      240
                                                                                      300
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taccgcggga tcgagccgac tttgccaaac tggttcgcgg tcacaaagac cagaaatggc
                                                                                      360
                                                                                      420
 gccggaggcg ggaacaaggt ggtggatgag tgctacatcc ccaattactt gctccccaaa
                                                                                      480
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                                                                                     540
                                                                                     600
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                                                                                     660
 tcagccaggt acatggagct ggtcgggtgg ctcgtggaca aggggattac ctcggagaag
                                                                                     720
 cagiggatec aggaggacca ggeeteatac ateteettea atgeggeete caactegegg
                                                                                     780
teccaaatea aggetgeett ggacaatgeg ggaaagatta tgageetgae taaaacegee
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cccgactacc tggtgggcca gcagcccgtg gaggacattt ccagcaatcg gatttataaa
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                                                                                    1020
                                                                                    1080
                                                                                    1140
                                                                                    1200
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1740
                                                                                    1800
ccagacgett geactgeetg egatetggte aatgtggatt tggatgaetg catetttgaa
                                                                                    1860
caataaatga tttaaatcag gtatggctgc cgatggttat cttccagatt ggctcgagga
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<223> Mutant rep DNA sequence: 511 GCA
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cgcgacttte tgacggaatg gcgccgtgtg agtaaggccc cggaggcct tttetttgtg caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccggggtg
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                                                                                    300
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt
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                                                                                    420
                                                                                    480
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1620

## -710-

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 cagiggatec aggaggacea ggeeteatae ateteettea atgeggeete caactegegg
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                                                                                                   1080
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<211> 1932
<212> DNA
<213> Artificial Sequence
<220>
<223> Mutant rep DNA sequence: 512 GCT
<400> 642
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                                                                                                  1080
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aagatgaccg ccaaggtcgt ggagtcggcc aaagccattc tcggaggaag caaggtgcgc
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                                                                                                  1320
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                                                                                                  1440
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                                                                                                  1560
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-711-

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1680
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tctgacatgg atctgaatct gattgagcag gcacccctga ccgtggccga gaagctgcag
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1140 1200

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<210> 647
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<220>

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  taccgeggga teggagegac tttgccaaac tggttegegg tcacaaagac cagaaatgge geeggaggeg ggaacaaggt ggtggatgag tgctacatec ecaattactt getececaaa acceagectg agetecagtg ggegtggact aatatggaac agtatttaag egeetgttg aateteacgg agegtaaacg gttggtggeg cagaatetga egeagetgte geagacgcag
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<223> Mutant rep DNA sequence: 598 GCA
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1920

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## -722-

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1260

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# -725-

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<sup>&</sup>lt;213> Artificial Sequence

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ccagacgett geactgeetg cgatetggte aatgeggatt tggatgaetg catetttgaa
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                                                                              840
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1740
                                                                             1800
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                                                                             1860
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<223> Mutant rep DNA sequence: 20 54 495 GCC GCC GCC

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1020

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-734-

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1680

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caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccggggtg
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1260

-737-

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1920

### -739-

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-740-

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1500

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goccaaatca aggotgoott ggacaatgog ggaaagatta tgagootgac taaaaccgoo
determination appropries against a superscript against a constant attention and the superscript against a constant against a co
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1080

### -744-

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<210> 691 <211> 1932

-745-

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<sup>&</sup>lt;213> Artificial Sequence

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-757-

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1740

### -758-

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#### -759-

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-760-

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